410 Rec'd PCT/PTO 13 SEP 2001

FORM PTO-1390 (Modified) (REV 11-2000) U.S. DEPARTMENT OF COMMERCE PATENT AND TRADEMARK OFFICE		ATTORNEY'S DOCKET NUMBER
TRANSMITTAL LETTER TO THE UNITED STATES DESIGNATED/ELECTED OFFICE (DO/EO/US) CONCERNING A FILING UNDER 35 U.S.C. 371		1038-1190 MIS:jb
		U.S. APPLICATION NO. (IF KNOWN, SEE 37 CFR) 09/936362
INTERNATIONAL APPLICATION NO. PCT/CA00/00289	INTERNATIONAL FILING DATE March 16, 2000	PRIORITY DATE CLAIMED March 16, 1999

TITLE OF INVENTION
RECOMBINANT HAEMOPHILUS INFLUENZAE ADHESIN PROTEINS

APPLICANT(S) FOR DO/EO/US
Sheena M. Loosmore; et al.

Applicant herewith submits to the United States Designated/Elected Office (DO/EO/US) the following items and other information:

1. ☒ This is a **FIRST** submission of items concerning a filing under 35 U.S.C. 371.
2. ☐ This is a **SECOND** or **SUBSEQUENT** submission of items concerning a filing under 35 U.S.C. 371.
3. ☐ This is an express request to begin national examination procedures (35 U.S.C. 371(f)). The submission must include items (5), (6), (9) and (24) indicated below.
4. ☐ The US has been elected by the expiration of 19 months from the priority date (Article 31).
5. ☒ A copy of the International Application as filed (35 U.S.C. 371 (c) (2))
   a. ☐ is attached hereto (required only if not communicated by the International Bureau).
   b. ☒ has been communicated by the International Bureau.
   c. ☐ is not required, as the application was filed in the United States Receiving Office (RO/US).
6. ☐ An English language translation of the International Application as filed (35 U.S.C. 371(c)(2)).
   a. ☐ is attached hereto.
   b. ☐ has been previously submitted under 35 U.S.C. 154(d)(4).
7. ☐ Amendments to the claims of the International Application under PCT Article 19 (35 U.S.C. 371 (c)(3))
   a. ☐ are attached hereto (required only if not communicated by the International Bureau).
   b. ☐ have been communicated by the International Bureau.
   c. ☐ have not been made; however, the time limit for making such amendments has NOT expired.
   d. ☐ have not been made and will not be made.
8. ☐ An English language translation of the amendments to the claims under PCT Article 19 (35 U.S.C. 371(c)(3)).
9. ☒ An oath or declaration of the inventor(s) (35 U.S.C. 371 (c)(4)). – unsigned copy
10. ☐ An English language translation of the annexes of the International Preliminary Examination Report under PCT Article 36 (35 U.S.C. 371 (c)(5)).
11. ☒ A copy of the International Preliminary Examination Report (PCT/IPEA/409).
12. ☒ A copy of the International Search Report (PCT/ISA/210).

Items 13 to 20 below concern document(s) or information included:

13. ☐ An Information Disclosure Statement under 37 CFR 1.97 and 1.98.
14. ☐ An assignment document for recording. A separate cover sheet in compliance with 37 CFR 3.28 and 3.31 is included.
15. ☒ A **FIRST** preliminary amendment.
16. ☐ A **SECOND** or **SUBSEQUENT** preliminary amendment.
17. ☐ A substitute specification.
18. ☐ A change of power of attorney and/or address letter.
19. ☐ A computer-readable form of the sequence listing in accordance with PCT Rule 13ter.2 and 35 U.S.C. 1.821 - 1.825.
20. ☐ A second copy of the published international application under 35 U.S.C. 154(d)(4).
21. ☐ A second copy of the English language translation of the international application under 35 U.S.C. 154(d)(4).
22. ☐ Certificate of Mailing by Express Mail
23. ☒ Other items or information:

Initial Information Data Sheet

Received: 9/13/01 1:44PM; 4165951163 -> Shoemaker & Mattare Ltd.; Page 3
SENT BY:SIMDAS ; 9-13-01 ; 2:22PM ; SIMDAS→ 7034150843;# 3
Rec'd PCT/PTO 13 SEP 2001

U.S. APPLICATION NO. (IF KNOWN, SEE 37 CFR 09/936362	INTERNATIONAL APPLICATION NO. PCT/CA00/00289	ATTORNEY'S DOCKET NUMBER 1038-1190 MIS:jb

24. The following fees are submitted:

	CALCULATIONS	PTO USE ONLY
BASIC NATIONAL FEE (37 CFR 1.492 (a) (1) - (5)) :		
☐ Neither international preliminary examination fee (37 CFR 1.482) nor international search fee (37 CFR 1.445(a)(2)) paid to USPTO and International Search Report not prepared by the EPO or JPO $1000.00		
☒ International preliminary examination fee (37 CFR 1.482) not paid to USPTO but International Search Report prepared by the EPO or JPO $860.00		
☐ International preliminary examination fee (37 CFR 1.482) not paid to USPTO but international search fee (37 CFR 1.445(a)(2)) paid to USPTO $710.00		
☐ International preliminary examination fee (37 CFR 1.482) paid to USPTO but all claims did not satisfy provisions of PCT Article 33(1)-(4) $690.00		
☐ International preliminary examination fee (37 CFR 1.482) paid to USPTO and all claims satisfied provisions of PCT Article 33(1)-(4) $100.00		
ENTER APPROPRIATE BASIC FEE AMOUNT =	$860.00	
Surcharge of $130.00 for furnishing the oath or declaration later than ☐ 20 ☐ 30 months from the earliest claimed priority date (37 CFR 1.492 (e)).	$0.00	

CLAIMS	NUMBER FILED	NUMBER EXTRA	RATE		
Total claims	29 - 20 =	9	x $18.00	$162.00	
Independent claims	6 - 3 =	3	x $80.00	$240.00	
Multiple Dependent Claims (check if applicable).			☒	$270.00	
TOTAL OF ABOVE CALCULATIONS =				$1,532.00	
☐ Applicant claims small entity status. (See 37 CFR 1.27). The fees indicated above are reduced by 1/2.				$0.00	
SUBTOTAL =				$1,532.00	
Processing fee of $130.00 for furnishing the English translation later than ☐ 20 ☐ 30 months from the earliest claimed priority date (37 CFR 1.492 (f)). +				$0.00	
TOTAL NATIONAL FEE =				$1,532.00	
Fee for recording the enclosed assignment (37 CFR 1.21(h)). The assignment must be accompanied by an appropriate cover sheet (37 CFR 3.28, 3.31) (check if applicable). ☒					
TOTAL FEES ENCLOSED =				$1532.00	
				Amount to be: refunded	$
				charged	$

a. ☐ A check in the amount of ____________ to cover the above fees is enclosed.

b. ☒ Please charge my Deposit Account No. 192253 in the amount of $1532.00 to cover the above fees. A duplicate copy of this sheet is enclosed.

c. ☒ The Commissioner is hereby authorized to charge any additional fees which may be required, or credit any overpayment to Deposit Account No. 192253 A duplicate copy of this sheet is enclosed.

d. ☐ Fees are to be charged to a credit card. WARNING: Information on this form may become public. **Credit card information should not be included on this form.** Provide credit card information and authorization on PTO-2038.

NOTE: Where an appropriate time limit under 37 CFR 1.494 or 1.495 has not been met, a petition to revive (37 CFR 1.137(a) or (b)) must be filed and granted to restore the application to pending status.

SEND ALL CORRESPONDENCE TO:

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24223
PATENT TRADEMARK OFFICE

[signature]
SIGNATURE

Michael I. Stewart
NAME

24,973
REGISTRATION NUMBER

September 11, 2001
DATE

INITIAL INFORMATION DATA SHEET

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Correspondence Customer Number: 24,223

Application Information

Title Line One:	RECOMBINANT HAEMOPHILUS INFLUENZAE
Title Line Two:	ADHESIN PROTEINS
Total Drawing Sheets:	204
Formal Drawings?:	Yes
Application Type:	Utility Patent
Docket Number:	1038-1190 MIS:jb

Representative Information

Registration Number: 24,973

Continuity Information

This application is a:	National Phase
Application One:	PCT/CA00/00289
Filing Date:	March 16, 2000

09/936362

518 Rec'd PCT/PTO ; 3 SEP 2001

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re National Phase of International

Appl'n. No.	:	PCT/CA00/00289
Filed	:	March 16, 2000
Applicant	:	Sheena M. Loosmore; et al.
Title	:	RECOMBINANT HAEMOPHILUS INFLUENZAE INFLUENZAE
Docket No.	:	1038-1190 MIS:jb

September 11, 2001

BY COURIER

The Commissioner of Patents
and Trademarks,
Washington, D.C. 20231,
U.S.A.

PRELIMINARY MENDMENT

Sir:

Please amend the above-identified application as follows:

In the Specification:

Before the first line of the specification, add the following:

" REFERENCE TO RELATED APPLICATIONS

This application is a national phase application under 35 U.S.C. 371 of PCT/CA00/00289."

REMARKS/ARGUMENTS

The specification has been amended on page 1 to reflect that this application is a U.S. National Phase filing under 35 U.S.C. 371 of PCT/CA00/00289.

Attached hereto is a marked-up version of the changes made to the specification by the current amendment. The attached page is captioned "**Version with markings to show changes made**."

Respectfully submitted,
SIM & McBURNEY

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Reg. No. 24,973

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Appl. No.

VERSION WITH MARKINGS TO SHOW CHANGES MADE

In the Specification:

Before the first line of the specification, add the following:

" REFERENCE TO RELATED APPLICATIONS

This application is a national phase application under 35 U.S.C. 371 of PCT/CA00/00289."

TITLE OF INVENTION

RECOMBINANT *HAEMOPHILUS INFLUENZAE* ADHESIN PROTEINS

REFERENCE TO RELATED APPLICATIONS

This application is a continuation-in-part of copending United States Patent Application No. 09/268,347.

FIELD OF INVENTION

The present invention relates to the field of molecular genetics and, in particular, to the production of recombinant *Haemophilus influenzae* adhesin (Hia) proteins.

BACKGROUND TO THE INVENTION

Haemophilus influenzae is the cause of several serious human diseases, such as meningitis, epiglottitis, septicemia and otitis media. There are six serotypes of *H. influenzae*, designated a to f, that are identified by their capsular polysaccharide. *H. influenzae* type b (Hib) was a major cause of bacterial meningitis until the introduction of several Hib conjugate vaccines in the 1980's (ref. 1. Throughout this application, various references are referred to in parenthesis to more fully describe the state of the art to which this invention pertains. Full bibliographic information for each citation is found at the end of the specification, immediately preceding the claims. The disclosures of these references are hereby incorporated by reference into the present disclosure). Vaccines based upon *H. influenzae* type b capsular polysaccharide conjugated to diphtheria toxoid (ref. 2), tetanus toxoid (ref. 3 and US patent 4,496,538), or *Neisseria meningitidis* outer membrane protein (ref. 4) have been effective in reducing *H. influenzae* type b-

induced meningitis. The other serotypes of *H. influenzae* are associated with invasive disease at low frequencies, although there appears to be an increase in the incidence in disease caused by these strains as the incidence of Hib disease declines (ref. 5; ref. 6). Non-encapsulated or non-typeable *H. influenzae* (NTHi) are also responsible for a wide range of human diseases including otitis media, epiglottitis, pneumonia, and tracheobronchitis. The incidence of NTHi-induced disease has not been affected by the introduction of the Hib vaccines (ref. 7).

Otitis media is the most common illness of early childhood, with 60 to 70% of all children, of less than 2 years of age, experiencing between one and three ear infections (ref. 8). Chronic otitis media is responsible for hearing, speech and cognitive impairments in children. *H. influenzae* infections account for about 30% of the cases of acute otitis media and about 60% of chronic otitis media. In the United States alone, treatment of otitis media costs between 1 and 2 billion dollars per year for antibiotics and surgical procedures such as tonsillectomies, adenoidectomies and insertion of tympanostomy tubes. It is estimated that an additional $30 billion is spent per annum on adjunct therapies, such as speech therapy and special education classes. Furthermore, many of the causative organisms of otitis media are becoming resistant to antibiotic treatment. An effective prophylactic vaccine against otitis media is thus desirable.

During natural infection by NTHi, surface-exposed outer membrane proteins that stimulate an antibody response are potentially important targets for bactericidal and/or protective antibodies and, therefore, potential vaccine candidates. A family of high molecular weight proteins (HMW1 and HMW2) that are important in attachment of NTHi to epithelial cells has been identified in about 70 to 75% of NTHi strains (ref. 9; ref. 10). These high molecular weight adhesins have been shown to afford some protection in the chinchilla model of otitis media (ref. 11). A second family of high molecular weight adhesion proteins has been identified in about 25% of NTHi and in encapsulated *H. influenzae* strains (ref. 12; ref. 13, ref. 14). The NTHi member of this second family is termed *Haemophilus influenzae* adhesin or Hia and the homologous protein found in encapsulated strains is termed *Haemophilus influenzae* surface fibril protein or Hsf. The *hia* gene was originally cloned from an expression library using convalescent sera from an otitis media patient, which indicates that it is an important immunogen during disease. The prototype Hia and Hsf proteins demonstrate about 82% sequence similarity, although the Hsf protein is considerably larger. The proteins are comprised of conserved amino and carboxy termini and several repeat motifs, with Hsf containing more repeat sequences than Hia. A high molecular weight protein (200 kDa) has also been identified from *Moraxella catarrhalis* that has some sequence homology with the Hsf and Hia proteins (U.S. Patent No. 5,808,024).

Since Hia or Hsf is conserved amongst encapsulated strains of *Haemophilus influenzae* and about 20 to 25% of non-encapsulated strains, and has been demonstrated to be an adhesin, the protein has utility in diagnosis of and vaccination against disease caused by *H. influenzae* or other bacterial pathogens that produce Hia or a protein capable of raising antibodies specifically reactive with Hia.

A disadvantage of Hia for use as an antigen in diagnosis, for the generation of anti-Hia antibodies useful in diagnosis and as an immunogen in vaccination is the low recovery of the native protein from *Haemophilus influenzae* species.

It would be advantageous to provide recombinant Hia protein for use as antigens, in immunogenic preparations including vaccines, carriers for other immunogens and in the generation of diagnostic reagents.

SUMMARY OF THE INVENTION

The present invention is directed towards the provision of recombinant *H. influenzae* adhesin (rHia) proteins.

In connection with the provision of such recombinant proteins, the present invention provides certain isolated and purified nucleic acid molecules. Accordingly, in one aspect thereof, the present invention provides an isolated and purified nucleic acid molecule encoding a *Haemophilus influenzae* adhesin (Hia) protein of a strain of *Haemophilus influenzae* having: (a) a DNA sequence selected from the group consisting of those shown in Figures 18, 19, 20, 21,

22, 23, 24 and 25 (SEQ ID Nos: 23, 25, 27, 29, 31, 33, 35, 37); or (b) a DNA sequence encoding a *Haemophilus influenzae* adhesin (Hia) protein having an amino acid sequence selected from the group consisting of those shown in Figures 18, 19, 20, 21, 22, 23, 24 and 25 (SEQ ID Nos: 24, 26, 28, 30, 32, 34, 36, 38).

Such nucleic acid may be included in a vector, which may be a plasmid vector. In particular, the nucleic acid molecule may encode the Hia protein from strain 11 or 33 of non-typeable *Haemophilus*.

In another aspect of the present invention, there is provided an isolated and purified nucleic acid molecule encoding an N-truncated *Haemophilus influenzae* adhesin (Hia) protein of a strain of *Haemophilus influenzae* which is amplifiable by a pair of nucleotides which are selected from the group consisting of SEQ ID No: 7 and SEQ ID No: 15; SEQ ID No: 9 and SEQ ID No: 15; SEQ ID No: 11 and SEQ ID No: 15; SEQ ID No: 13; SEQ ID No: 15; SEQ ID No: 49; and SEQ ID No: 51.

Such nucleic acid may be included in a vector, which may be a plasmid vector. In particular, the nucleic acid molecule may encode an N-truncated Hia protein from strain 11 or 33 of non-typeable *Haemophilus*, starting at codon V38 or S44.

The plasmid vector incorporating the isolated and purified nucleic acid provided in accordance with these aspects of the invention may have the identifying characteristics of a plasmid which is selected from the group consisting of:

DS-2008-2-3 as shown in Figure 1A

DS-2186-1-1 as shown in Figure 5A

DS-2201-1 as shown in Figure 5A

DS-2186-2-1 as shown in Figure 5A

DS-2168-2-6 as shown in Figure 5A

1A-191-3-1 as shown in Figure 32

The vector provided herein may include the *cer* gene from *E. coli*. Accordingly, in another aspect of the present invention, there is provided a vector for transforming a host, comprising a nucleic acid molecule encoding a full-length or N-truncated *Haemophilus influenzae* adhesin (Hia) protein, a promoter for expression of said full-length or truncated Hia protein and, optionally, the *cer* gene of *E. coli*. The vector may be a plasmid vector or other non-replicating vector, which may have the identifying characteristics of a plasmid vector which is selected from the group consisting of:

BK-96-2-11 as shown in Figure 6A

DS-2242-1 as shown in Figure 7A

DS-2242-2 as shown in Figure 7A

DS-2340-2-3 as shown in Figure 8A

DS-2447-2 as shown in Figure 9A

DS-2448-17 as shown in Figure 9B

JB-2930-3 as shown in Figure 32

The vectors provided herein may comprise a replicating vector, including a vector from *Salmonella*, BCG, adenovirus, poxvirus, vaccinia or poliovirus.

Any of the vectors provided herein may be employed to transform a suitable host cell for expression therein of a protective *Haemophilus influenzae* adhesin (Hia) protein of a non-typeable strain of *Haemophilus*,

which may be in full-length or truncated form. Such host conveniently may be *E. coli*. Such expression may be under the control of the T7 promoter and expression of the recombinant Hia from the transformed host may be effected by culturing in an inducing concentration of lactose or other convenient inducing agent.

The present invention further includes, in a further aspect thereof, a recombinant protective *Haemophilus influenzae* adhesin (Hia) protein of a non-typeable *Haemophilus* strain producible by the transformed host, particularly *E. coli*, provided herein. Such Hia protein may be provided in the form of an immunogenic fragment or adhesin-functional analog of the recombinant protein.

The recombinant Hia proteins, full-length or N-truncated, provided herein are useful as antigens in immunogenic compositions, carriers for other immunogens, diagnostic agents and in the generation of diagnostic agents. The nucleic acid molecules which encode the Hia protein, full-length or N-truncated, also are useful as probes for diagnostic use and also in immunogenic compositions.

The present invention, in an additional aspect thereof, provides an immunogenic composition, comprising at least one immunologically active component which is selected from the group consisting of an isolated and purified nucleic acid molecule as provided herein and a recombinant protective Hia protein, full-length or N-truncated, of a strain of *Haemophilus*, as provided herein, and a pharmaceutically-acceptable carrier therefor.

The immunogenic compositions provided herein may be formulated as a vaccine for *in vivo* administration to a host to provide protection against disease caused by *H. influenzae*. For such purpose, the compositions may be formulated as a microparticle, capsule, ISCOM or liposome preparation. The immunogenic composition may be provided in combination with a targeting molecule for delivery to specific cells of the immune system or to mucosal surfaces.

The immunogenic compositions of the invention (including vaccines) may further comprise at least one other immunogenic or immunostimulating material and the immunostimulating material may be at least one adjuvant or at least one cytokine. Suitable adjuvants for use in the present invention include (but are not limited to) aluminum phosphate, aluminum hydroxide, QS21, Quil A, derivatives and components thereof, ISCOM matrix, calcium phosphate, calcium hydroxide, zinc hydroxide, a glycolipid analog, an octadecyl ester of an amino acid, a muramyl dipeptide, polyphosphazene, ISCOPREP, DC-chol, DDBA and a lipoprotein and other adjuvants.

Advantageous combinations of adjuvants are described in copending United States Patent Application Serial No. 08/261,194 filed June 16, 1994 and 08/483,856 filed June 7, 1995, assigned to the assignee hereof and the disclosure of which is incorporated herein by reference (WO 95/34308 published November 21, 1995).

In accordance with another aspect of the invention, there is provided a method for generating an immune response in a host, comprising the step of

administering to a susceptible host an effective amount of the immunogenic composition as recited above. The immune response may be humoral or a cell-mediated immune response. Hosts in which protection against disease may be conferred include primates, including humans.

In accordance with other aspects of the invention, there is provided the immunogenic compositions provided herein when used as a medicament and the use of these components of the immunogenic compositions in the manufacture of an immunogenic composition.

The present invention includes, in a yet additional aspect thereof, a method for the production of a protective *Haemophilus influenzae* adhesin (Hia) protein of a non-typeable strain of *Haemophilus influenzae*, which comprises:

transforming a host, such as *E. coli*, with a vector comprising a nucleic acid molecule encoding an N-truncated form of the *Haemophilus influenzae* adhesin protein as provided herein,

growing the host to express the encoded truncated Hia, and

isolating and purifying the expressed Hia protein.

The encoded truncated Hia may be expressed in inclusion bodies. The isolation and purification step may be effected by disrupting the grown transformed cells to produce a supernatant and the inclusion bodies containing the Hia, solubilizing the inclusion bodies after separation from the supernatant, to produce a solution of the recombinant Hia, chromatographically purifying the solution of recombinant Hia free from

cell debris, and isolating the purified recombinant Hia protein.

The vector transforming the host cell, such as *E. coli*, may include the T7 promoter and the *E. coli* or other host cell may be cultured in the presence of an inducing amount of lactose or other convenient inducing agent.

The strain of *Haemophilus influenzae* herein may be selected from the group of non-typeable strains consisting of strains 11, 33, 32, 29, M4071, K9, K22 and 12. Specific nucleic acid sequences for the genes encoding the respective Hia proteins from such strains are provided herein and are described below.

The nucleic acid molecules provided herein are useful in diagnostic applications. Accordingly, in a further aspect of the invention, there is provided a method of determining the presence, in a sample, of nucleic acid encoding a *Haemophilus influenzae* adhesin protein, comprising the steps of:

a) contacting the sample with a nucleic acid molecule as provided herein to produce duplexes comprising the nucleic acid molecule provided herein are nucleic acid encoding the Hia protein of a strain of *Haemophilus* present in the sample and specifically hybridizable therewith; and

b) determining the production of the duplexes.

In addition, the present invention provides a diagnostic kit for determining the presence, in a sample, of nucleic acid encoding a *Haemophilus influenzae* adhesin protein, comprising:

a) a nucleic acid molecule as provided herein;

b) means for contacting the nucleic acid molecule with the sample to produce duplexes comprising the nucleic acid molecule and any such nucleic acid molecule; and

c) means for determining production of the duplexes.

The recombinantly produced truncated Hia proteins provided herein also are useful in diagnostic applications. Accordingly, in another aspect of the invention, there is provided a method of determining the presence of antibodies specifically reactive with the Hia protein in a sample, comprising the steps of (a) contacting the sample with the recombinant Hia protein provided herein to provide complexes of the recombinant Hia protein and any such antibodies present in the sample specifically reactive therewith; and (b) determining production of the complexes.

Advantages of the present invention include:

- an isolated and purified nucleic acid molecule encoding a *Haemophilus influenzae* adhesin protein or a fragment or an analog of the Hia protein;
- recombinantly-produced Hia proteins, free from any other *Haemophilus* proteins; and
- diagnostic kits and immunological reagents for specific identification of *Haemophilus*.

BRIEF DESCRIPTION OF DRAWINGS

The present invention will be further understood from the following description with reference to the drawings, in which:

Figure 1A shows a restriction map for plasmid DS-2008-2-3 that contains the T7 promoter and the full-length NTHi strain 11 *hia* gene.

Figure 1B shows the oligonucleotides used to PCR amplify the strain 11 *hia* gene. Sense Strand (5038.SL): SEQ ID No: 1, encoded amino acids SEQ ID No: 2; Antisense Strand (5039.SL): SEQ ID No: 3, complement SEQ ID No: 4, encoded amino acids SEQ ID No: 5. Restriction enzyme sites are: B, *BamH* I; Bg, *Bgl* II; H, *Hind* III; N, *Nde* I; Ps, *Pst* I; Sty, *Sty* I. Other abbreviations are: T7p, T7 promoter; ApR, ampicillin resistance.

Figure 2 shows an immunoblot of the recognition of full-length rHia protein by anti-native *Moraxella catarrhalis* high molecular weight adhesin antibody. Lane 1, DS-2043-1 uninduced; lane 2, DS-2043-1, induced for 4h; lane 3, DS-2043-2 uninduced; lane 4, DS-2043-2, induced for 4h; lane 5, molecular weight markers. DS-2043-1 and DS-2043-2 are independent clones of *pT7 hia(11)* in BL21 (DE3).

Figure 3 shows the construction of plasmids DS-2092-1 and DS-2092-40 that contain tandem copies of the *T7 hia* gene cassette for the strain 11 *hia* gene. Restriction enzyme sites are: B, *BamH* I; Bg, *Bgl* II; H, *Hind* III; Ps, *Pst* I; Xb, *Xba* I. Other abbreviations are: CAP, calf alkaline phosphatase; T7p, T7 promoter; ApR, ampicillin resistance.

Figure 4 shows the sites of truncation for the strain 11 Hia protein (SEQ ID No: 6).

Figure 5A shows the construction of plasmids expressing truncated *hia* genes from strain 11.

Restriction enzyme sites are: B, *BamH* I; Bg, *Bgl* II; H, *Hind* III; N, *Nde* I; Nhe, *Nhe* I; Ps, *Pst* I; R, *EcoR* I; Sty, Sty I; Xb, *Xba* I. Other abbreviations are: T7p, T7 promoter; ApR, ampicillin resistance; KanR, kanamycin resistance.

Figure 5B shows the oligonucleotides used to PCR amplify the 5'-fragments for the truncated genes. E21 truncation: Sense (5524.SL): SEQ ID No: 7, encoded amino acids SEQ ID No: 8; T33 truncation: Sense (5525.SL) SEQ ID No: 9, encoded amino acids SEQ ID No: 10; V38 truncation: Sense (5526.SL): SEQ ID No: 11, encoded amino acids, SEQ ID No: 12; N52 truncation: Sense (5527.SL): SEQ ID No: 13, encoded amino acids SEQ ID No: 14; Antisense (5528.SL): SEQ ID No: 15; complement SEQ ID No: 16, encoded amino acids SEQ ID No: 17.

Figure 6A shows the construction of plasmid BK-96-2-11 that contains the V38 *hia* gene from NTHi strain 11 and the *E. coli cer* gene. Restriction enzyme sites are: B, *BamH* I; Bg, *Bgl* II; K, *Kpn* I; N, *Nde* I; P, *Pst* I; R, *EcoR* I; S, *Sal* I; Sm, *Sma* I; Sty, *Sty* I; Xb, *Xba* I; Xho, *Xho* I. Other abbreviations are: T7p, T7 promoter; ApR, ampicillin resistance; KanR, kanamycin resistance; CAP, calf alkaline phosphatase; tt1 transcription terminator 1 from *trpA*; tt2, transcription terminator 2 from T7 gene 10.

Figure 6B shows the oligonucleotides used to construct the multiple cloning site and transcription terminators. "R" and "Ps" indicate termini that will overlap with EcoR I or Pst I ends, but will not re-

generate the sites. Upperstrand (SEQ ID No.: 50) lower strand (SEQ ID No.: 51).

Figure 7A shows the construction of plasmids DS-2242-1 and DS-2242-2 that contain the T7 promoter and full-length NTHi strain 33 *hia* gene, the *E. coli cer* gene and the kanamycin resistance gene. Restriction enzyme sites are: A, *AlwN* I; B, *BamH* I; Bg, *Bgl* II; H, *Hind* III; K, *Kpn* I; N, *Nde* I; Ps, *Pst* I; R, *EcoR* I; S, *Sal* I; Sm, *Sma* I; Xb, *Xba* I; Xho, *Xho* I. Other abbreviations are: T7p, T7 promoter; ApR, ampicillin resistance; KanR, kanamycin resistance; tt1, transcription terminator 1 from *trpA*; tt2, transcription terminator 2 from T7 gene 10.

Figure 7B shows the oligonucleotides used to generate the 5'-end of the strain 33 *hia* gene coding strand (SEQ ID No.: 52), complementary strand (SEQ ID No.: 53), and encoded amino acid sequence (SEQ ID No.: 54).

Figure 8A shows the construction of plasmid DS-2340-2-3 that contains the T7 promoter and the V38 *hia* gene from strain 33, the *E. coli cer* gene and the kanamycin resistance gene. Restriction enzyme sites are: B, *BamH* I; Bg, *Bgl* II; H, *Hind* III; N, *Nde* I; Ps, *Pst* I; R, *EcoR* I; S, *Sal* I; Sn, *SnaB* I; Xb, *Xba* I. Other abbreviations are: T7p, T7 promoter; ApR, ampicillin resistance; KanR, kanamycin resistance; tt1, transcription terminator 1 from *trpA*; tt2, transcription terminator 2 from T7 gene 10.

Figure 8B shows the oligonucleotides used to PCR amplify the 5'-end of the truncated *hia* gene. Sense (6286.SL): SEQ ID No: 60, encoded amino acids SEQ ID

No: 61; antisense (6287.SL) SEQ ID No: 18, complement SEQ ID No: 19, encoded amino acids SEQ ID No: 20.

Figures 9A and 9B show the construction of plasmids DS-2447-2 and DS-2448-17, that contain tandem copies of the *T7 V38 hia (11)* and *T7 V38 hia (33)* genes, respectively. Restriction enzyme sites are: B, BamH I; Bg, Bgl II; H, Hind III; Ps, Pst I; R, EcoR I; S, Sal I; Xb, Xba I. Other abbreviations are: T7p, T7 promoter; ApR, ampicillin resistance; KanR, kanamycin resistance; CAP, calf alkaline phosphatase; tt1, transcription terminator 1 from trpA; tt2, transcription terminator 2 from T7 gene 10.

Figure 10 shows the expression of rHia. Panel A: lane 1, full-length rHia (11) no induction; lane 2, full-length rHia (11); lane 3, E21 rHia (11); lane 4, T33 rHia (11); lane 5, V38 rHia (11); lane 6, N52 rHia (11). Panel B: lane 1, V38 rHia (11) no induction; lane 2, V38 rHia (11); lane 3, V38 rHia (11)/cer.

Figure 11 shows a purification scheme for rHia proteins. Abbreviations are: SP, supernatant; PPT, precipitate; DTT, dithiothreitol; OG, octyl glucoside; (x) means discarded.

Figure 12, having panels A and B, shows the SDS-PAGE analysis of purified rHia. Panel A shows purified V38 rHia protein from strain 11 and panel B shows purified V38 rHia protein from strain 33. Lane 1, molecular weight markers; lane 2, whole-cell lysate; lane 3, crude extract; lane 4, purified rHia protein.

Figure 13, having panels A, B and C, shows the stability of V38 rHia (11). Panel A shows samples stored at 4°C without glycerol. Panel B shows samples

stored at 4°C, in the presence of 20% glycerol. Panel C shows samples stored at -20°C in the presence of 20% glycerol. Lane 0 indicates t_0; lanes 1 to 8 indicate samples stored for 1 to 8 weeks.

Figure 14, having panels A and B, shows the immunogenicity of V38 rHia (11) or V38 rHia (33) in CD-1 mice. Panel A shows the response after a single immunization and panel B shows the response of a prime/boost immunization.

Figures 15A and 15B show the immunogenicity of V38 rHia (11) in BALB/c mice and guinea pigs. Figure 15A shows the antibody response in mice and Figure 15B shows the response in guinea pigs.

Figure 16 illustrates the protective ability of V38 rHia (33) against nasopharyngeal colonization in a chinchilla model.

Figure 17 shows the oligonucleotides used to PCR amplify additional *hia* genes. Sense (5040.SL), SEQ ID No: 21, encoded amino acids SEQ ID No: 22; Antisense (5039.SL), SEQ ID No: 3, complement SEQ ID No: 4, encoded amino acids SEQ ID No: 5.

Figure 18 shows the nucleotide sequence (SEQ ID No: 23) and deduced amino acid sequence (SEQ ID No: 24) of the *hia* gene from NTHi strain 33.

Figure 19 shows the nucleotide sequence (SEQ ID No: 25) and deduced amino acid sequence (SEQ ID No: 26) of the hia gene from NTHi strain 32.

Figure 20 shows the nucleotide sequence (SEQ ID No: 27) and deduced amino acid sequence (SEQ ID No: 28) of the *hia* gene from NTHi strain 29.

Figure 21 shows the nucleotide sequence (SEQ ID No: 29) and deduced amino acid sequence (SEQ ID No: 30 of the *hia* gene from NTHi strain M4071.

Figure 22 shows the nucleotide sequence (SEQ ID No: 31) and deduced amino acid sequence (SEQ ID No: 32) of the *hia* gene from NTHi strain K9.

Figure 23 shows the nucleotide sequence (SEQ ID No: 33) and deduced amino acid sequence (SEQ ID No: 34) of the *hia* gene from NTHi strain K22.

Figure 24 shows the nucleotide sequence (SEQ ID No: 35) and deduced amino acid sequence (SEQ ID No: 36) of the *hia* gene from type c strain API.

Figure 25 shows the nucleotide sequence (SEQ ID No: 37) and deduced amino acid sequence (SEQ ID No: 38) of the *hia* locus from NTHi strain 12. The overlined or underlined sequences indicate oligonucleotides used to PCR amplify across the junction of the two *orfs*. Sense (6431.SL) SEQ ID No: 39, (6432.SL) SEQ ID No: 40; antisense (6295.SL) SEQ ID No: 41, (6271.SL) SEQ ID No: 42.

Figure 26 shows the nucleotide sequence (SEQ ID No.: 43) and deduced amino acid sequence (SEQ ID No.: 44) of the *hia* locus from NTHi strain 11, as published in U.S. Patent No. 5,646,259.

Figure 27 shows the alignment of the upstream ORF from the strain 12 *hia* locus (SEQ ID No: 45) with part of the HI1732 protein (SEQ ID No: 46) from *H. influenzae* type b strain Rd.

Figure 28 shows the alignment of amino acid sequences from Hia (SEQ ID Nos. 24, 26, 28, 34, 30, 44, 32), Hsf (SEQ ID No.: 47) and partial sequences from

Moraxella catarrhalis high molecular weight proteins (200 kDa) from strains 4223 and LES-1 (SEQ ID Nos.: 48, 49). Asterisks within sequences indicate stop codons, but below the sequence they indicated sequence homology. Dots indicate identical residues. The sequence alignments were prepared by direct comparison of the amino acid sequences of the respective proteins.

Figure 29 shows the oligonucleotides used to PCR amplify the 5' end of the hia gene at the S44 truncated position. Sense (6817.SL) SEQ ID No: 55, encoding amino acids SEQ ID No: 56; antisense (6818.SL) SEQ ID No: 57, complement SEQ ID No: 58, encoded amino acids SEQ ID No: 59.

Figure 30 shows the construction of plasmid JB-2930-3 that contains the S44 *hia* gene from NTHi strain 11 and the E. coli *car* gene and the T7 promoter. Restriction enzyme sites are: B, *BamH* I; Bg, *Bgl* II; K, *Kpn* I; N, *Nde* I; P, *Pst* I; R, *EcoR* I; S, *Sal* I; Sm, *Sma* I; Sty, *Sty* I; Xb, *Xba* I; Xho, *Xho* I. Other abbreviations are: T7p, T7 promoter; ApR, ampicillin resistance; KanR, kanamycin resistance; CAP, calf alkaline phosphatase; tt1 transcription terminator 1 from *trpA*; tt2, transcription terminator 2 from T7 gene 10.

Figure 31 shows SDS-PAGE analysis of the expression of rHia from S44. Lane 1, expression from pET S44 vector at time 0 (no induction); lane 2 expression from pET S44 vector after 4 hours induction; lane 3 expression from JB-2930-3 after 4 hours induction.

Figures 32 shows a schematic representation of the two vectors used for the expression study, JB-2930-3 and IA-191-3-1, of S44-truncated rHia.

GENERAL DESCRIPTION OF THE INVENTION

Since *H. influenzae* strains produce low quantities of the Hia and Hsf proteins, the *hia* gene from NTHi strains was cloned into an expression vector for overproduction of the recombinant protein in *E. coli*. When the full-length recombinant Hia (rHia) protein was expressed, it was made in relatively low quantities. In order to confirm that there was expression of the recombinant protein, an immunoblot was performed using antibody raised to a *Moraxella catarrhalis* high molecular weight adhesin protein identified as 200 kDa in US Patent No. 5,808,024, assigned to the assignee and the disclosure of which is incorporated herein by reference. Antibody against the gel-purified native 200 kDa protein recognized a specific induced band in the rHia protein sample. The yield of rHia was not significantly improved by increasing the gene copy number of the T7 *hia* gene cassette.

The *E. coli cer* gene has been shown to stabilize plasmids containing large inserts (ref. 15), but the yield of rHia was not significantly improved by adding the *E. coli cer* gene to the expression vector. However, the *E. coli* cells were observed to clump during culture, suggesting that there was surface expression of the Hia adhesin protein. The apparent toxicity of the rHia protein might be overcome if it were made as inclusion bodies, so truncations were made at the 5'-end of the gene to delete putative signal

sequences. This modification resulted in good production and recovery of truncated rHia starting from the V38 position.

The full-length and V38-truncated rHia proteins were immunogenic and the resultant anti-rHia antibodies were protective in passive infant rat models of bacteremia due to *H. influenzae* type a or type b strains. In addition, the truncated V38 rHia protein was found to be partially protective against nasopharyngeal colonization in an active challenge model in chinchillas. The protection afforded by rHia derived from an NTHi strain against disease caused by NTHi and encapsulated type a or type b strains, indicates that there may be common protective epitopes. The cloning and sequence analysis of additional *hia* genes may help to identify conserved regions. The full-length or N-terminal truncated rHia proteins may be used as vaccine components to protect against *Haemophilus influenzae* disease.

Any *Haemophilus* strains that have *hia* genes may be conveniently used to provide the purified and isolated nucleic acid molecules (which may be in the form of DNA molecules), comprising at least a portion coding for a Hia protein as typified by embodiments of the present invention. Such strains are generally available from clinical sources and from bacterial culture collections, such as American Type Culture Collection. Appropriate strains of *Haemophilus* include:

Non-typeable *Haemophilus* strain 11;

Non-typeable *Haemophilus* strain 33;

Non-typeable *Haemophilus* strain 32;

Non-typeable *Haemophilus* strain 29;

Non-typeable *Haemophilus* strain M4071;

Non-typeable *Haemophilus* strain K9;

Non-typeable *Haemophilus* strain K22;

Non-typeable *Haemophilus* strain 12;

Type C *Haemophilus* strain API.

In this application, the term "Hia" protein is used to define a family of Hia proteins that includes those having naturally occurring variations in their amino acid sequences as found in various strains of *Haemophilus*.

Referring to Fig. 1A, there is illustrated a restriction map of plasmid DS-2008-2-3 that contains a full-length *hia* gene from non-typeable *Haemophilus influenzae* strain 11, under the influence of the T7 promoter. The nucleic acid (SEQ ID No.: 43) and deduced amino acid sequence (SEQ ID No.: 44) of the *hia* gene from strain 11, are described in the aforementioned U.S. Patent No. 5,646,259 (and identified therein as "HA1"). The oligonucleotides used to PCR amplify the *hia* gene from the ATG start codon of the gene of strain 11 are shown in Fig. 1B.

Referring to Fig. 2, there is illustrated an immunoblot demonstrating the recognition of the rHia (11) protein by anti-native *Moraxella catarrhalis* high molecular weight adhesin antibody. The *M. catarrhalis* high molecular weight adhesin or 200 kDa protein described in the aforementioned US Patent No. 5,808,024 has some sequence homology with the Hia and Hsf proteins, especially at the carboxy terminus (Fig. 28).

Referring to Fig. 3, there is illustrated a construction scheme for plasmids DS-2092-1 and DS-2092-40 that contain tandem copies of T7 *hia* gene cassettes comprising the full-length *hia* gene from NTHi strain 11. Such plasmids that contain increased copy numbers of genes often have enhanced production levels for recombinant proteins. However, as seen below, the low yield of recombinant Hia was not significantly improved by increasing the gene copy number.

Referring to Fig. 4, there is illustrated the N-terminal sequence of the NTHi strain 11 protein and the position of time N-terminally truncated rHia proteins. The N-terminal truncation up to position E21 deletes a long hydrophobic region that may constitute part of a signal sequence for Hia. The deletion up to position T33 includes a long hydrophobic region and follows a potential Ala-X-Ala signal cleavage site. The deletion up to position V38 includes a long hydrophobic region and follows a potential Ala-X-Ala signal cleavage site. The recombinant Hia protein starting at position S44 includes a long hydrophobic region and follows a potential Ala-X-Ala signal cleavage site. The recombinant Hia protein starting at position N52 mimics the approximate start of the related high molecular weight (200 kDa) adhesin from *Moraxella catarrhalis* described in the aforementioned US Patent No. 5,808,024, which recombinant protein is over-produced if truncated at its N-terminus to start at V56.

Referring to Fig. 5A, there is illustrated the construction scheme for the generation of plasmids DS-2186-1-1, DS-2201-1, DS-2186-2-1, and DS-2168-2-6

producing four of the N-terminal truncated rHia proteins. The oligonucleotides used to PCR amplify the 5'-fragments are shown in Fig. 5B. In Figure 30, there is illustrated the construction scheme for the generation of plasmids JB-2930-3, which produces the S44 deletion. The oligonucleotides used to PCR amplify the 5'-fragments are shown in Figure 29.

Referring to Fig. 6A, there is illustrated a construction scheme for the generation of plasmid BK-96-2-11 that contains the V38 *hia* gene from NTHi strain 11 as well as the *E. coli cer* gene that has been shown to stabilize plasmids. The introduction of the *cer* gene into plasmids producing toxic proteins, was predicted to enhance protein production. There was an observed change in the morphology of the *E. coli* cells producing full-length rHia in the presence of the *cer* gene, in that they clumped. This suggests that there was enhanced expression of the adhesin at the surface of the cells that caused the clumping. The expression plasmid BK-96-2-11 also contains transcription terminators upstream and downstream of the T7 V38 *hia* gene cassette that were predicted to enhance the gene stability. The oligonucleotides used to generate the multiple cloning site and transcription terminators are shown in Fig. 6B.

Referring to Fig. 7A, there is illustrated a construction scheme for plasmids DS-2242-1 and DS-2242-2 that contain a full-length *hia* gene from non-typeable *Haemophilus influenzae* strain 33, under the influence of the T7 promoter. The expression plasmids also contain the *E. coli cer* gene and transcription

terminators upstream and downstream of the T7 *hia* (33) gene cassette. DS-2242-1 has the terminators coded on the same strand as the T7 *hia* (33) gene. However, there was no observable difference in the expression of rHia from the two plasmids. The oligonucleotides used to construct the authentic 5'-end of the NTHi strain 33 gene are shown in Fig. 7B.

Referring to Fig. 8A, there is illustrated a construction scheme for plasmid DS-2340-2-3 that contains the V38 *hia* gene from NTHi strain 33 as well as the *E. coli cer* gene. There are also transcription terminators located upstream and downstream of the T7 V38 *hia* gene cassette, on the same strand. The oligonucleotides used to PCR amplify the NTHi strain 33 *hia* gene from the V38 codon, are shown in Fig. 8B.

Referring to Fig. 9, there is shown the construction of plasmids DS-2447-2 and DS-2448-17 that contain tandem copies of the *T7 V38 hia (11)* or *T7 V38 hia (33)* gene cassettes, respectively.

Referring to Fig. 10, panel A, there is illustrated the production of rHia proteins from plasmids encoding full-length or truncated *hia* genes from NTHi strain 11. The production of the full-length rHia (11) protein was very low. There was also low expression observed for the E21 and T33 truncated rHia proteins. However, the V38 and N52 truncated rHia proteins have significantly improved expression levels. As shown in Fig. 10, panel B, the production of V38 rHia (11) appears to be enhanced when the *E. coli cer* gene is added to the expression plasmid.

Referring to Fig. 11, there is illustrated a purification scheme for rHia proteins, produced as inclusion bodies. Cells were lysed by sonication and the inclusion bodies purified by serial extractions. The inclusion bodies were solubilized in guanidinium chloride and impurities precipitated by the addition of polyethlyene glycol (PEG). Addition of $(NH_4)_2SO_4$ resulted in precipitation of rHia and the crude rHia was further purified by gel filtration.

Referring to Fig. 12, there is illustrated the purified V38 rHia proteins from strains 11 and 33. The inclusion bodies are shown in lane 3 and the final purified protein in lane 4. The estimated purity of the purified protein is greater than about 90% as determined by SDS-PAGE densitometry.

Referring to Fig. 13, there is shown the SDS-PAGE analysis of the stability of rHia proteins produced as described herein during 8 weeks of storage with or without glycerol at 4°C and with glycerol at -20°C. The protein is stable under any of these conditions.

Referring to Fig. 14, there is illustrated the immunogenicity of V38 rHia proteins from strains 11 and 33 in CD-1 mice. At doses from 0.3 to 10 μg, there is a strong immune response after one or two doses with either protein. There is no obvious dose response at these levels. Similar results were observed in BALB/c mice (Fig. 15A) and in guinea pigs (Fig. 15B), indicating that rHia was very immunogenic, even at 0.3 μg per dose.

Referring to Fig. 16, there is illustrated the protection afforded by V38 rHia (33) against

colonization by NTHi strain 33. As described by Yang et al (ref. 20), a chinchilla nasopharyngeal colonization model has been developed to assess protection against this earliest stage of disease. The model was initially established for NTHi strains that express *hmw* genes and had to be adapted for NTHi strains expressing *hia* genes. For the prototype *hmw*-expressing strain (NTHi 12), 10^2 to 10^8 cfu could be used to establish infection, but 5 x 10^8 cfu of NTHi strain 33 was required, and even at this high level no infection could be established with the prototype *hia*-expressing strain 11. At a 100 µg dose, it is evident that there is partial protection in the immunized cohort, although there is no protection at a 50 µg dose. Such protection against the early stages of disease illustrates the utility of the rHia adhesins as vaccine antigens.

Referring to Fig. 17, there is illustrated the oligonucleotides used to PCR amplify additional *Haemophilus influenzae hia* genes. The sequences are based upon the conserved amino and carboxy terminal sequences of the Hia and Hsf proteins.

Referring to Fig. 18, there is illustrated the complete nucleotide sequence and deduced amino acid sequence of the NTHi strain 33 *hia* gene. Referring to Fig. 19, there is illustrated the complete nucleotide sequence and deduced amino acid sequence of the NTHi strain 32 *hia* gene. Referring to Fig. 20, there is illustrated the complete nucleotide sequence and deduced amino acid sequence of the NTHi strain 29 *hia* gene. Referring to Fig. 21, there is illustrated the

complete nucleotide sequence and deduced amino acid sequence of the NTHi strain M4071 *hia* gene. Referring to Fig. 22, there is illustrated the complete nucleotide sequence and deduced amino acid sequence of the NTHi strain K9 *hia* gene. Referring to Fig. 23, there is illustrated the complete nucleotide sequence and deduced amino acid sequence of the NTHi strain K22 *hia* gene. Referring to Fig. 24, there is illustrated the complete nucleotide sequence and deduced amino acid sequence of the *Haemophilus influenzae* type c strain API *hia* gene. Referring to Fig. 25, there is illustrated the complete nucleotide sequence and deduced amino acid sequence of the *hia* locus from NTHi strain 12. The PCR amplified fragment contains the 3'-end of a gene related to HI1733 gene of the *Haemophilus influenzae* type d strain Rd genome joined to the 3'-end of an *hia* gene. An alignment of the upstream ORF with the HI1733 protein is shown in Fig. 27.

Figure 26 shows the complete nucleotide sequence and the deduced amino acid sequence of the *Hia* gene from NTHi strain 11, as published in the aforementioned USP 5,646,259.

Referring to Fig. 28, there is illustrated an alignment of the deduced protein sequences from Hsf, Hia, and partial sequences of the *M. catarrhalis* 200 kDa protein.

It is clearly apparent to one skilled in the art, that the various embodiments of the present invention have use in applications in the fields of vaccination, diagnosis, treatment of *Haemophilus* infection and the generation of immunological agents. A further non-

limiting discussion of such uses is further presented below.

Vaccine Preparation and Use

Immunogenic compositions, suitable to be used as vaccines, may be prepared from immunogenic recombinant *Haemophilus influenzae* adhesin (rHia) proteins of non-typeable *Haemophilus* strains, immunogenic analogs and fragments thereof and/or immunogenic peptides as disclosed herein. The vaccine elicits an immune response which produces antibodies, including anti-rHia antibodies and antibodies that are opsonizing or bactericidal.

Immunogenic compositions, including vaccines, may be prepared as injectables, as liquid solutions or emulsions. The rHia protein, immunogenic analogs and fragments thereof and/or immunogenic peptides may be mixed with pharmaceutically acceptable excipients which are compatible with the rHia protein, immunogenic fragments analogs or immunogenic peptides. Such excipients may include, water, saline, dextrose, glycerol, ethanol and combinations thereof.

The immunogenic compositions and vaccines may further contain auxiliary substances such as wetting or emulsifying agents, pH buffering agents, or adjuvants to enhance the effectiveness of the vaccines.

Immunogenic compositions and vaccines may be administered parenterally, by injection subcutaneously or intramuscularly. Alternatively, the immunogenic compositions formed according to the present invention, may be formulated and delivered in a manner to evoke an immune response at mucosal surfaces. Thus, the

immunogenic composition may be administered to mucosal surfaces by, for example, the nasal or oral (intragastric) routes.

The immunogenic composition may be provided in combination with a targeting molecule for delivery to specific cells of the immune system or to mucosal surfaces. Some such targeting molecules include vitamin B12 and fragments of bacterial toxins, as described in WO 92/17167 (Biotech Australia Pty. Ltd.), and monoclonal antibodies, as described in U.S. Patent No. 5,194,254 (Barber et al).

Alternatively, other modes of administration including suppositories and oral formulations may be desirable. For suppositories, binders and carriers may include, for example polyalkalene glycols or triglycerides. Oral formulations may include normally employed incipients such as, for example pharmaceutical grades of saccharine, cellulose and magnesium carbonate. These compositions take the form of solutions, suspensions, tablets, pills, capsules, sustained release formulations or powders and contain about 1 to 95% of the rHia protein, fragment analogs and/or peptides.

The vaccines are administered in a manner compatible with the dosage formulation, and in such amount as will be therapeutically effective, protective and immunogenic. The quantity to be administered depends on the subject to be treated, including, for example, the capacity of the individual's immune system to synthesize antibodies, and if needed, to produce a cell-mediated immune response. Precise amounts of

active ingredient required to be administered depend on the judgment of the practitioner. However, suitable dosage ranges are readily determinable by one skilled in the art and may be of the order of micrograms of the rHia, analogs and fragments thereof and/or peptides. Suitable regimes for initial administration and booster doses are also variable, but may include an initial administration followed by subsequent administrations. The dosage of the vaccine may also depend on the route of administration and will vary according to the size of the host.

The nucleic acid molecules encoding the rHia proteins of non-typeable *Haemophilus* may also be used directly for immunization by administration of the DNA directly, for example by injection for genetic immunization or by constructing a live vector, such as *Salmonella*, BCG, adenovirus, poxvirus, vaccinia or poliovirus, containing the nucleic acid molecule. A discussion of some live vectors that have been used to carry heterologous antigens to the immune system is contained in, for example, O'Hagan (1992) (ref. 16). Processes for the direct injection of DNA into test subjects for genetic immunization are described in, for example, Ulmer et al., 1993 (ref. 17).

Immunogenicity can be significantly improved if the antigens are co-administered with adjuvants, commonly used as an 0.05 to 1.0 percent solution in phosphate - buffered saline. Adjuvants enhance the immunogenicity of an antigen but are not necessarily immunogenic themselves. Adjuvants may act by retaining the antigen locally near the site of administration to

produce a depot effect facilitating a slow, sustained release of antigen to cells of the immune system. Adjuvants can also attract cells of the immune system to an antigen depot and stimulate such cells to elicit immune responses.

Immunostimulatory agents or adjuvants have been used for many years to improve the host immune responses to, for example, vaccines. Intrinsic adjuvants, such as lipopolysaccharides, normally are the components of the killed or attenuated bacteria used as vaccines. Extrinsic adjuvants are immunomodulators which are typically non-covalently linked to antigens and are formulated to enhance the host immune responses. Thus, adjuvants have been identified that enhance the immune response to antigens delivered parenterally. Some of these adjuvants are toxic, however, and can cause undesirable side-effects, making them unsuitable for use in humans and many animals. Indeed, only aluminum hydroxide and aluminum phosphate (collectively commonly referred to as alum) are routinely used as adjuvants in human and veterinary vaccines. The efficacy of alum in increasing antibody responses to diphtheria and tetanus toxoids is well established.

A wide range of extrinsic adjuvants can provoke potent immune responses to antigens. These include the specific adjuvants detailed above as well as saponins complexed to membrane protein antigens (immune stimulating complexes), pluronic polymers with mineral oil, killed mycobacteria and mineral oil, Freund's complete adjuvants, bacterial products, such as muramyl

dipeptide (MDP) and lipopolysaccharide (LPS), as well as lipid A, and liposomes.

To efficiently induce humoral immune responses (HIR) and cell-mediated immunity (CMI), immunogens are emulsified in adjuvants. Many adjuvants are toxic, inducing granulomas, acute and chronic inflammations (Freund's complete adjuvant, FCA), cytolysis (saponins and pluronic polymers) and pyrogenicity, arthritis and anterior uveitis (LPS and MDP). Although FCA is an excellent adjuvant and widely used in research, it is not licensed for use in human or veterinary vaccines because of its toxicity.

Desirable characteristics of ideal adjuvants include:

(1) lack of toxicity;

(2) ability to stimulate a long-lasting immune response;

(3) simplicity of manufacture and stability in long-term storage;

(4) ability to elicit both CMI and HIR to antigens administered by various routes, if required;

(5) synergy with other adjuvants;

(6) capability of selectively interacting with populations of antigen presenting cells (APC);

(7) ability to specifically elicit appropriate T_H1 or T_H2 cell-specific immune responses; and

(8) ability to selectively increase appropriate antibody isotype levels (for example, IgA) against antigens.

US Patent No. 4,855,283 granted to Lockhoff et al on August 8, 1989 which is incorporated herein by

reference thereto teaches glycolipid analogues including N-glycosylamides, N-glycosylureas and N-glycosylcarbamates, each of which is substituted in the sugar residue by an amino acid, as immuno-modulators or adjuvants. Thus, Lockhoff et al. 1991 (ref. 18) reported that N-glycolipid analogs displaying structural similarities to the naturally-occurring glycolipids, such as glycosphingolipids and glycoglycerolipids, are capable of eliciting strong immune responses in both herpes simplex virus vaccine and pseudorabies virus vaccine. Some glycolipids have been synthesized from long chain-alkylamines and fatty acids that are linked directly with the sugars through the anomeric carbon atom, to mimic the functions of the naturally occurring lipid residues.

U.S. Patent No. 4,258,029 granted to Moloney, assigned to the assignee hereof and incorporated herein by reference thereto, teaches that octadecyl tyrosine hydrochloride (OTH) functions as an adjuvant when complexed with tetanus toxoid and formalin inactivated type I, II and III poliomyelitis virus vaccine. Also, Nixon-George et al. 1990 (ref. 19), reported that octadecyl esters of aromatic amino acids complexed with a recombinant hepatitis B surface antigen, enhanced the host immune responses against hepatitis B virus.

Immunoassays

The rHia protein of a non-typeable strain of *Haemophilus*, analogs and fragments thereof produced according to the present invention are useful as immunogens, as antigens in immunoassays including enzyme-linked immunosorbent assay (ELISA), RIAs and

other non-enzyme linked antibody binding assays or procedures known in the art for the detection of anti-bacterial, *Haemophilus*, and/or Hia antibodies. In ELISA assays, the Hia protein, analogs and fragments are immobilized onto a selected surface, for example a surface capable of binding proteins or peptides, such as the wells of a polystyrene microtiter plate. After washing to remove incompletely adsorbed Hia protein, analogs and/or fragments, a nonspecific protein such as a solution of bovine serum albumin (BSA) or casein that is known to be antigenically neutral with regard to the test sample may be bound to the selected surface. This allows for blocking of nonspecific adsorption sites on the immobilizing surface and thus reduces the background caused by nonspecific bindings of antisera onto the surface.

The immobilizing surface is then contacted with a sample, such as clinical or biological materials, to be tested in a manner conducive to immune complex (antigen/antibody) formation. This may include diluting the sample with diluents, such as BSA, bovine gamma globulin (BGG) and/or phosphate buffered saline (PBS)/Tween. The sample is then allowed to incubate for from about 2 to about 4 hours, at temperature such as of the order of about 25° to about 37°C. Following incubation, the sample-contacted surface is washed to remove non-immunocomplexed material. The washing procedure may include washing with a solution such as PBS/Tween, or a borate buffer.

Following formation of specific immunocomplexes between the test sample and the bound Hia protein,

analogs and/or fragments, and subsequent washing, the occurrence, and even amount, of immunocomplex formation may be determined by subjecting the immunocomplex to a second antibody having specificity for the first antibody. If the test sample is of human origin, the second antibody is an antibody having specificity for human immunoglobulins and in general IgG. To provide detecting means, the second antibody may have an associated activity, such as an enzymatic activity, that will generate, for example, a color development, upon incubating with an appropriate chromogenic substrate. Quantification may then achieved by measuring the degree of color generation using, for example, a visible spectra spectrophotometer.

Use of Sequences as Hybridization Probes

The nucleotide sequences of the present invention, comprising the newly-isolated and characterized sequences of the *hia* genes, allow for the identification and cloning of the *hia* genes from other non-typeable strains of *Haemophilus*.

The nucleotide sequences comprising the sequence of *hia* genes of the present invention are useful for their ability to selectively form duplex molecules with complementary stretches of other *hia* genes. Depending on the application, a variety of hybridization conditions may be employed to achieve varying degrees of selectivity of the probe toward the other *hia* genes in other strains of non-typeable *Haemophilus*. For a high degree of selectivity, relatively stringent conditions are used to form the duplexes, such as low salt and/or high temperature conditions, such as

provided by 0.02 M to 0.15 M NaCl at temperatures of between about 50°C to 70°C. For some applications, less stringent hybridization conditions are required such as 0.15 M to 0.9 M salt, at temperatures ranging from between 20°C to 55°C. Hybridization conditions can also be rendered more stringent by the addition of increasing amount of formamide, to destabilize the hybrid duplex. Thus, particular hybridization conditions can be readily manipulated, and will generally be a method of choice depending on the desired results. In general, convenient hybridization temperatures in the presence of 50% formamide and 0.15 M NaCl are: 42°C for an *hia* gene which is about 95 to 100% homologous to the target nucleic acid fragment, 37°C for about 90 to 95 homology and 32°C for about 85 to 90% homology.

In a clinical diagnostic embodiment, the nucleic acid sequences of the *hia* genes of the present invention may be used in combination with an appropriate means, such as a label, for determining hybridization. A wide variety of appropriate indicator means are known in the art, including radioactive, enzymatic or other ligands, such as avidin/biotin, which are capable of providing a detectable signal. In some diagnostic embodiments, an enzyme tag, such as urease, alkaline phosphatase or peroxidase, instead of a radioactive tag may be used. In the case of enzyme tags, colorimetric indicator substrates are known which can be employed to provide a means visible to the human eye or spectrophotometrically, to identify specific

hybridization with samples containing *Hia* genes sequences.

The nucleic acid sequences of *Hia* genes of the present invention are useful as hybridization probes in solution hybridizations and in embodiments employing solid-phase procedures. In embodiments involving solid-phase procedures the test DNA (or RNA) from samples, such as clinical samples, including exudates, body fluids (e.g., serum, amniotic fluid, middle ear effusion, sputum, bronchoalveolar lavage fluid) or even tissues, is adsorbed or otherwise affixed to a selected matrix or surface. The fixed, single-stranded nucleic acid is then subjected to specific hybridization with selected probes comprising the nucleic acid sequences of the *hia* genes or fragments thereof of the present invention under desired conditions. The selected conditions will depend on the particular circumstances based on the particular criteria required depending on, for example, the G+C contents, type of target nucleic acid, source of nucleic acid, size of hybridization probe etc. Following washing of the hybridization surface so as to remove non-specifically bound probe molecules, specific hybridization is detected, or even quantified, by means of the label. It is preferred to select nucleic acid sequence portions which are conserved among species of *Haemophilus*. The selected probe may be at least 18 bp in length and may be in the range of 30 bp to 90 bp long.

Expression of the *Haemophilus influenzae* adhesin Genes

Plasmid vectors containing replicon and control sequences which are derived from species compatible

with the host cell may be used for the expression of the *hia* genes in expression systems. The vector ordinarily carries a replication site, as well as marking sequences which are capable of providing phenotypic selection in transformed cells. For example, *E. coli* may be transformed using pBR322 which contains genes for ampicillin and tetracycline resistance and thus provides easy means for identifying transformed cells. The pBR322 plasmid, or other microbial plasmid or phage, must also contain, or be modified to contain, promoters which can be used by the host cell for expression of its own proteins.

In addition, phage vectors containing replicon and control sequences that are compatible with the host can be used as a transforming vector in connection with these hosts. For example, the phage in lambda GEM™-11 may be utilized in making recombinant phage vectors which can be used to transform host cells, such as *E. coli* LE392.

Promoters commonly used in recombinant DNA construction include the β-lactamase (penicillinase) and lactose promoter systems and other microbial promoters, such as the T7 promoter system employed herein in preferred embodiments (U.S. Patent 4,952,496). Details concerning the nucleotide sequences of promoters are known, enabling a skilled worker to ligate them functionally with genes. The particular promoter used will generally be a matter of choice depending upon the desired results. Hosts that are appropriate for expression of the Hia protein and immunological fragments or analogs thereof include *E.*

coli, *Bordetella* species, *Bacillus* species, *Haemophilus*, fungi, yeast or the baculovirus expression system may be used. *E. coli* is the preferred host used herein.

In accordance with this invention, it is preferred to produce the Hia proteins by recombinant methods, particularly when the naturally occurring Hia protein as purified from a culture of a species of *Haemophilus* may include trace amounts of toxic materials or other contaminants. This problem can be avoided by using recombinantly produced Hia protein in heterologous systems which can be isolated from the host in a manner to minimize contaminants in the purified materials, specifically employing the constructs described herein.

BIOLOGICAL DEPOSITS

A vector that contains nucleic acid coding for a high molecular weight protein of a non-typeable strain of *Haemophilus* that is described and referred to herein has been deposited with the America Type Culture Collection (ATCC) located at 10801 University Boulevard, Manassas, Virginia 20110-2209, USA, pursuant the Budapest Treaty and prior to the filing of this application. Samples of the deposited vector will become available to the public and all restrictions imposed or access to the deposits will be received upon grant of a patent based on this United States patent application. In addition, the deposit will be replaced if viable samples cannot be dispensed by the Depository. The invention described and claimed herein is not limited in scope by the biological materials deposited, since the deposited embodiment is intended

only as an illustration of the invention. Any equivalent or similar vectors that contain nucleic acid which encodes equivalent or similar antigens as described in this application are within the scope of the invention.

Deposit Summary

Plasmid	ATCC	Deposit Date
BK-96-2-11	203771	February 11, 1999

EXAMPLES

The above disclosure generally describes the present invention. A more complete understanding can be obtained by reference to the following specific Examples. These Examples are described solely for purposes of illustration and are not intended to limit the scope of the invention. Changes in form and substitution of equivalents are contemplated as circumstances may suggest or render expedient. Although specific terms have been employed herein, such terms are intended in a descriptive sense and not for purposes of limitations.

Methods of molecular genetics, protein biochemistry, immunology and fermentation technology used, but not explicitly described in this disclosure and these Examples, are amply reported in the scientific literature and are well within the ability of those skilled in the art.

Example 1

This Example describes the construction of plasmid DS-2008-2-3 that expresses full-length rHia proteins from NTHi strain 11.

Chromosomal DNA was purified from NTHi strain 11 and the full-length *hia* gene was PCR amplified using the oligonucleotides (5038.SL and 5039.SL) described in Figure 1B. An Nde I site was engineered at the 5'-end of the gene and a BamH I site was engineered at the 3'-end for cloning into the pT7-7 expression vector (ref. 21). The amplified fragment was digested with Nde I/BamH I and cloned into pT7-7 that had been digested with the same enzymes. Plasmid DS-2008-2-3 contains a 3.4 kb strain 11 *hia* gene downstream of the T7 promoter (Fig. 1A). The plasmid was used to express recombinant Hia (Example 9 below).

Example 2

This Example illustrates the recognition of rHia by anti-native *Moraxella catarrhalis* high molecular weight adhesin antibody.

There is some sequence conservation observed between the *Haemophilus influenzae* Hia proteins and a *Moraxella catarrhalis* high molecular weight adhesin identified as the *M. catarrhalis* 200 kDa protein in aforementioned US Patent No. 5,808,024 (Fig. 28). The native *M. catarrhalis* 200 kDa protein was gel purified as described in US Patent No. 5,808,024 and guinea pig anti-native 200 kDa antibody was generated. The T7 *hia* gene was expressed from plasmid DS-2008-2-3 and the cell culture containing the rHia protein was electroblotted to nitrocellulose membrane. Immunoblot analysis using anti-native 200 kDa antibody showed that the antibody recognized the rHia protein, as seen in Figure 2.

Example 3

This Example describes the construction of plasmids DS-2092-1 and DS-2092-40 that contain tandem copies of *T7 hia* (11) gene cassettes.

In order to improve the production of full-length recombinant Hia protein, tandem copies of the *T7 hia* gene cassette containing the strain 11 *hia* gene (Example 1) were inserted into a single vector. Plasmid DS-2008-2-3 was linearized with *Bgl* II and dephosphorylated. Plasmid DS-2008-2-3 was also digested with *Bgl* II and *BamH* I to excise the *T7 hia* gene cassette. The *T7 hia* fragment was ligated into the linearized vector to generate plasmid DS-2092-1 that contains two copies of the *T7 hia* gene in the anti-clockwise orientation (a,a) and plasmid DS-2092-40 that contains tandem copies in opposite orientations (a,c) (Fig. 3). There was no obvious improvement in expression of rHia from either construct (see Example 9 below).

Example 4

This Example describes the construction of plasmids expressing truncated strain 11 *hia* genes.

The production of the rHia protein from single or tandem copies of the *T7 hia* gene cassette was very low and the protein seemed to be toxic to *E. coli* (as described below in Example 9). Since *H. influenzae* Hia is a surface-exposed adhesin molecule, it must either utilize a signal sequence or accessory protein(s) for secretion, but there are no known accessory genes involved. If the signal sequence were removed for expression of the recombinant protein in *E. coli*, the

rHia might be expressed as inclusion bodies and the toxic effect reduced. A putative signal sequence and cleavage sites were identified and four constructs expressing N-terminally truncated rHia proteins were designed (Fig. 4). There is a unique *Sty* I site in the strain 11 *hia* gene about 500 bp from the start codon. Plasmid DS-2008-2-3 was digested with *Nde* I and *Sty* I and the 5.7 kb vector fragment purified (Fig. 5A). PCR primers were designed to amplify from the truncation site to the *Sty* I site and a unique *Nhe* I site was introduced into the antisense primer for screening truncated clones (Fig. 5B). The amplified fragments were subcloned into pCRII for easier manipulation, generating plasmids DS-2153R-1-2 (E21), DS-2165-4-8 (T33), DS-2153-3-5 (V38), and DS-2153-4-4 (N52). The pCRII *hia* plasmids were digested with *Nde* I and *Sty* I and the fragments ligated with the vector piece from DS-2008-2-3. Plasmids DS-2186-1-1 (E21), DS-2201-1 (T33), DS-2186-2-1 (V38), and DS-2168-2-6 (N52) were generated that contained the T7 promoter and truncated *hia* genes as indicated in parentheses. These plasmids were used to express recombinant Hia (see Example 9 below).

Example 5

This Example describes the construction of plasmid BK-96-2-11 that contains the *T7 V38 hia (11)* cassette, the *E. coli cer* gene, and the kanamycin resistance gene.

Plasmid DS-1843-2 is a pBR328-based plasmid in which a multiple cloning site and two transcription terminators have been introduced on oligonucleotides,

between the *EcoR* I and *Pst* I sites, thus destroying both the chloramphenicol and ampicillin resistance genes (Fig. 6B). The kanamycin resistance gene from pUC-4K was inserted at the *Sal* I site, to generate plasmid DS-2147-1 that is kanamycin resistant and tetracycline sensitive. Plasmid DS-2224-1-4 is a pUC plasmid containing a synthetic *E. coli cer* gene (ref. 15) constructed from oligonucleotides and flanked by *BamH* I sites. The 290 bp *BamH* I fragment of the *cer* gene was inserted into the *BamH* I site of DS-2147-1 creating plasmid BK-2-1-2. This pBR-based plasmid thus contains a multiple cloning site, the kanamycin resistance gene and the *cer* gene. Plasmid BK-2-1-2 was linearized with *Bgl* II and dephosphorylated. Plasmid DS-2186-2-1 was digested with *Bgl* II and *BamH* I and the 3.6 kb *T7 V38 hia* fragment was inserted into BK-2-1-2, creating plasmid BK-96-2-11 (Fig. 6A).

Example 6

This Example describes the construction of plasmids DS-2242-1 and DS-2242-2 that express the full-length NTHi strain 33 *hia* gene in the presence of the *E. coli cer* gene.

Chromosomal DNA was purified from NTHi strain 33 and PCR amplification was performed using oligonucleotides 5039.SL and 5040.SL (Fig. 17). The sense primer (5040.SL) was designed based upon the 5'-flanking sequence of strain 11 *hia* and the conserved amino terminal sequences of the NTHi Hia and Hib Hsf proteins. The antisense primer (5039.SL) was the same as that described in Example 1 and was based upon the conserved carboxy terminal sequences of the Hia and Hsf

proteins. The 3 kb strain 33 *hia* PCR fragment was cloned into pCR II, generating plasmid DS-1917-3-8.

In order to express the full-length strain 33 *hia* gene, approximately 106 bp of the 5'-end of the gene was synthesized from oligonucleotides, from the start codon to an *AlwN* I site (Fig. 7B). Plasmid DS-1917-3-8 was digested with *AlwN* I and *BamH* I and the approximately 2.9 kb fragment containing the *hia* gene was purified. Plasmid pT7-7 was digested with *Nde* I and *BamH* I. The *Nde* I - *AlwN* I oligonucleotides and *AlwN* I - *BamH* I *hia* fragment were ligated into the pT7-7 vector, generating plasmid DS-2103-4.

In order to include the *E. coli cer* gene and utilize kanamycin selection, the *Bgl* II - *BamH* I fragment containing the *T7 hia (33)* gene cassette was excised from DS-2103-4 and cloned into BK-2-1-1 that had been digested with *Bgl* II and dephosphorylated. Plasmids DS-2242-1 and DS-2242-2 contain single copies of the *T7 hia (33)* gene cassette in opposite orientations, the *E. coli cer* gene, and the kanamycin resistance gene (Fig. 7A).

Example 7

This Example describes the construction of plasmid DS-2340-2-3 that contains a *T7 hia* gene cassette with a truncated V38 strain 33 *hia* gene, the *E. coli cer* gene, and the kanamycin resistance gene.

PCR primers were designed to amplify a 250 bp fragment of the 5'-end of the NTHi strain 33 hia gene from a V38 start codon up to an internal *SnaB* I site. An *Nde* I site was added at the 5'-end for cloning purposes and the fragment was amplified using plasmid

DS-2242-1 as template. The construction scheme is shown in Figure 8A and the PCR primers are shown in Figure 8B. The fragment was cloned into pCR II generating plasmid DS-2328-1-1. DS-2242-1 was digested with *Nde* I and *SnaB* I and the 8.5 kb vector fragment purified. DS-2328-1-1 was digested with *Nde* I and *SnaB* I and the 0.25 kb 5' *hia* fragment was ligated with the 8.5 kb vector fragment from DS-2242-1, to generate plasmid DS-2340-2-3.

Example 8

This Example illustrates the construction of plasmids DS-2447-2 and DS-2448-17 that contain tandem copies of *T7 V38 hia (11)* or *T7 V38 hia (33)* gene cassettes, respectively, the *E. coli cer* gene, and a kanamycin resistance gene.

Plasmid BK-96-2-11, that contains a *T7 V38 hia (11)* gene cassette, was linearized with *Bgl* II and dephosphorylated. The *Bgl* II-*BamH* I *T7 V38 hia (11)* gene cassette from DS-2186-2-1 was ligated into BK-96-2-11, generating plasmid DS-2447-2 that contains tandem copies of the *T7 V38 hia (11)* gene in the same orientation (Fig. 9A).

Plasmid DS-2340-2-3 was digested with *EcoR* I and the *T7 V38 hia (33)* gene cassette was subcloned into pUC-BgXb that had been digested with *EcoR* I and dephosphorylated. The resultant plasmid, DS-2440-2 was digested with *Bgl* II and *BamH* I to release the *T7 V38 hia (33)* cassette that was ligated with DS-2340-2-3 that had been linearized with *Bgl* II and dephosphorylated. Plasmid DS-2448-17 contains tandem *T7 V38 hia(33)* genes in the same orientation (Fig. 9B).

Example 9

This Example illustrates the expression of full-length and truncated recombinant *hia* genes.

DNA from expression plasmids prepared as described in the preceding Examples, was introduced into electrocompetent *E. coli* BL21 (DE3) cells using a BioRad electroporator. Cells were grown at 37°C in NZCYM medium using the appropriate antibiotic selection to A_{578} of 0.3 before the addition of lactose to 1.0% for 4 hours. Samples were adjusted to 0.2 OD/µl with SDS-PAGE lysis + loading buffer and the same amount of each protein sample was loaded onto SDS-PAGE gels (ref. 22). Figure 10 illustrates the relative production of rHia (11) proteins from various constructs. As seen in panel A, there is an increase in production with decreased size of rHia. V38- (lane 5) and N52-truncated rHia (lane 6) have significantly higher expression levels than their longer counterparts (lanes 2, 3, 4). In addition, panel B demonstrates that the production of V38 rHia is apparently increased in the presence of the *cer* gene.

Example 10

This Example illustrates the purification of rHia proteins.

All the recombinant Hia proteins were expressed as inclusion bodies in *E. coli* and were purified by the same procedure (Fig.11). *E. coli* cell pellets from 500 ml culture were resuspended in 50 ml of 50 mM Tris-HCl, pH 8.0, containing 0.1 M NaCl, and disrupted by sonication. The extract was centrifuged at 20,000 *g* for 30 min and the resultant supernatant was discarded.

The pellet (PPT_1) was further extracted, in 50 ml of 50 mM Tris-HCl, pH 8.0 containing 0.5% Triton X-100 and 10 mM EDTA, then centrifuged at 20,000 *g* for 30 min, and the supernatant was discarded. The pellet (PPT_2) was further extracted in 50 ml of 50 mM Tris-HCl, pH 8.0, containing 1% octylglucoside, then centrifuged at 20,000 *g* for 30 min, and the supernatant was discarded.

The resultant pellet (PPT_3) obtained after the above extractions contains the inclusion bodies. The pellet was solubilized in 6 ml of 50 mM Tris-HCl, pH 8.0, containing 6 M guanidine and 5 mM DTT. Twelve ml of 50 mM Tris-HCl, pH 8.0 was added to this solution and the mixture was centrifuged at 20,000 *g* for 30 min. The supernatant (SUP_4) was precipitated with polyethylene glycol (PEG) 4000 at a final concentration of 7%. The resultant pellet (PPT_5) was removed by centrifugation at 20,000 *g* for 30 min and the supernatant was precipitated by $(NH_4)_2SO_4$ at 50% saturation. The $(NH_4)_2SO_4$ precipitate was collected by centrifugation at 20,000 *g* for 30 min. The resultant pellet (PPT_6) was dissolved in 2 ml of 50 mM Tris-HCl, pH 8.0, containing 6 M guanidine HCl and 5 mM DTT and the clear solution was purified on a Superdex 200 gel filtration column equilibrated in 50 mM Tris-HCl, pH 8.0, containing 2 M guanidine HCl. The fractions were analysed by SDS-PAGE and those containing the purified rHia were pooled and dialysed overnight at 4°C against PBS, then centrifuged at 20,000 *g* for 30 min. The protein remained soluble under these conditions and glycerol was added to the rHia preparation at a final concentration of 20% for storage at -20°C. SDS-PAGE

analysis of purified V38 rHia (11) and V38 rHia (33) is illustrated in Figure 12. The average yield of the purified V38 rHia proteins is about 10 mg L^{-1} culture.

In order to study the stability of rHia, the purified V38 rHia (11) protein was stored at 4°C with or without glycerol and at -20°C with glycerol. The protein was found to be stable under all three conditions and remained intact for at least eight weeks with repeated freezing and thawing (Fig. 13).

Example 11

This Example illustrates the immunogenicity of V38 rHia (11) and V38 rHia (33) proteins.

Hyperimmune antisera against rHia proteins were produced by immunizing two guinea pigs (Charles River) intramuscularly (i.m.) with 5 µg doses of antigen emulsified in complete Freund's adjuvant (CFA, Difco) on day 1. Animals were boosted on days 14 and 28 with 5 µg doses of protein in incomplete Freund's adjuvant (IFA) and sera were collected on day 42. Anti-Hib strain MinnA and anti- *Haemophilus* type a strain ATCC 9006 antisera were generated using the same protocol, except that a heat-inactivated bacterial preparation was used as the immunogen ($1x10^8$ cfu per dose).

To study the immunogenicity of the V38 rHia proteins, groups of five CD-1 mice (Charles River, Quebec) were immunized s.c. on days 1 and 28 with 0.3, 1, 3, and 10 µg of antigen, in the presence of $AlPO_4$ (alum) (1.5 mg per dose). Blood samples were collected on days 1, 28 and 42. Mice generated significant anti-V38 rHia antibody responses even with a single injection of 0.3 µg antigen (Fig. 14, panel A),

suggesting that both proteins had retained immunogenicity after inclusion body extraction and solubilization. No statistically significant difference was found in the antibody titers induced by the V38 rHia proteins derived from strains 11 or 33.

To study the immunogenicity of the V38 rHia (11) protein in BALB/c mice, groups of five animals (Charles River, Quebec) were immunized s.c. on days 1, 28 and 42 with 0.3, 1, 3, and 10 µg of antigen, in the presence of $AlPO_4$ (1.5 mg per dose). Blood samples were collected on days 1, 14, 28, 42 and 56. High antibody titers were observed in all groups, indicating that the protein is very immunogenic even at 0.3 µg per dose (Fig. 15, panel A).

To study the immunogenicity of the V38 rHia (11) protein in guinea pigs, groups of five animals (Charles River, Quebec) were immunized s.c. on days 1, 28 and 42 with 0.3, 1, 3, and 10 µg of antigen, in the presence of $AlPO_4$ (1.5 mg per dose). Blood samples were collected on days 1, 14, 28, 42 and 56. High antibody titers were observed in all groups, indicating that the protein is also very immunogenic in guinea pigs (Fig. 15, panel B).

Example 12

This Example illustrates the analysis of the protection afforded by anti-rHia antibodies in passive infant rat models of bacteremia.

Pregnant Wistar rats were purchased from Charles River. In the *H. influenzae* type b bacteremia model, groups of 6 to 10 five-day old infant rats were injected s.c. in the dorsal region with 0.1 ml of

guinea pig anti-rHia or anti-strain MinnA antiserum. The control animals received injections with pre-immune sera only. Twenty hours later, the animals were challenged intraperitoneally (i.p.) with 200 to 240 colony-forming units (cfu) of freshly grown Hib strain MinnA (0.1 ml). Blood samples were collected 20 h post-challenge, via cardiac puncture under isoflurane anesthesia and plated on chocolate agar plates. Colonies were counted after one day and the results were statistically analyzed by Fisher's Exact test.

In the *H. influenzae* type a bacteremia model (ref. 23), groups of 9 to 10 five-day old infant rats were injected s.c. in the dorsal region with 0.1 ml of guinea pig anti-rHia or anti-strain ATCC 9006 antiserum. The animals in the control group were injected with guinea pig pre-immune serum. Twenty hours later, the animals were challenged i.p. with 100,000 cfu of freshly grown *H. influenzae* type a strain ATCC 9006 (0.1 ml). Blood samples were collected 20 h post-challenge and analysed as described above.

As shown in Tables 1 and 2 below, the infant rats that were passively immunized with either guinea pig anti-rHia (11) or anti-V38 rHia (11) antisera, were all significantly protected against type a or type b *H. influenzae* caused bacteremia. These results demonstrate that antibodies raised to the slightly truncated Hia protein (V38 rHia) are as efficacious as those raised to the full-length protein at protecting animals against bacteremia caused by type a or type b *H. influenzae*. Such protection afforded by an NTHi-derived recombinant protein against invasive disease

caused by encapsulated bacteria, illustrates the utility of the rHia proteins as vaccine antigens.

Example 13

This Example illustrates the protection afforded by immunization with V38 rHia protein in a chinchilla model of nasopharyngeal colonization.

A nasopharyngeal colonization model has been described by Yang et al (ref. 20). The model works well for those NTHi strains that produce the HMW adhesins, but reproducible colonization could not be established with Hia-producing strains under the same conditions. Repeated attempts to colonize with the prototype Hia-producing NTHi strain 11, were unsuccessful. Colonization was achieved with NTHi strain 33 at 5 x 10^8 cfu per inoculum, compared with only 10^6 cfu required for the prototype HMW-producing NTHi strain 12. Under these conditions, partial protection was observed in animals immunized with 100 µg of V38 rHia (33) and challenged with the homologous NTHi strain 33.

Example 14

This Example illustrates the cloning and sequence analysis of additional *hia* genes from *H. influenzae* strains.

Oligonucleotides (5040.SL and 5039.SL) for PCR amplification were designed based upon the conserved promoter, N-terminal and C-terminal sequences of the *hia* and *hsf* genes and proteins (Fig. 17). The strains chosen for PCR amplification were chosen based upon their reactivity with anti-rHia (11) antisera.

Chromosomal DNA was prepared from NTHi strains 12, 29, 32, M4071, K9 and, K22 and *Haemophilus* type c strain API. PCR amplification was performed as follows: each reaction mixture contained 5 to 100 ng of DNA, 1 µg of each primer, 5 units of taq+ or tsg+ (Sangon) or taq plus long (Stratagene), 2 mM dNTPs, 20 mM Tris-HCl (pH 8.8), 10 mM KCl, 10 mM $(NH_4)_2SO_4$, 2 mM $MgSO_4$, 0.1% Triton X-100, BSA. Cycling conditions were: 95°C for 1 min, followed by 25 cycles of 95°C for 30 sec, 45°C for 1 min, 72°C for 2 min; then 72°C for 10 min.

The nucleotide and deduced amino acid sequences of the *hia* gene from strain 33 are shown in Figure 18. The predicted Hia protein from strain 33 has a molecular weight of 103.6 kDa and a pI of 9.47. The nucleotide and deduced amino acid sequences of the *hia* gene from strain 32 are shown in Figure 19. The predicted Hia protein from strain 32 has a molecular weight of 70.4 kDa and a pI of 5.67. There is a KDEL sequence present between residues 493 and 496. Such sequences have been associated with anchoring proteins to the endoplasmic reticulum. The deduced strain 32 Hia protein is significantly smaller and has a significantly different pI, however it does contain many of the motifs present in other Hia molecules.

The nucleotide and deduced amino acid sequences of the *hia* gene from strain 29 are shown in Figure 20. The predicted Hia protein from strain 29 has a molecular weight of 114.4 kDa and a pI of 7.58. The nucleotide and deduced amino acid sequences of the *hia* gene from strain K22 are shown in Figure 23. The predicted Hia protein from strain K22 has a molecular weight of 114.4

kDa and a pI of 7.58. The deduced Hia sequences from NTHi strains 29 and K22 were found to be identical. Strain 29 was isolated from a 7-month old child with otitis media in Cleveland, Ohio, while strain K22 was isolated from an aborigine near Kimberly, Australia.

The nucleotide and deduced amino acid sequences of the *hia* gene from strain 4071 are shown in Figure 21. The predicted Hia protein from strain M4071 has a molecular weight of 103.4 kDa and a pI of 9.49. There is a KDEL sequence present between residues 534 and 537.

The nucleotide and deduced amino acid sequences of the *hia* gene from strain K9 are shown in Figure 22. The predicted Hia protein from K9 has a molecular weight of 113.8 kDa and a pI of 6.45.

The nucleotide and deduced amino acid sequences of the *hia* gene from strain type c *Haemophilus* API are shown in Figure 24. The predicted Hia protein from API has a molecular weight of 249.4 kDa and a pI of 5.34. The deduced Hia/Hsf sequence from the type c strain API is nearly identical to the published type b Hsf sequence except for a 60 residue insert. Since the NTHi-based Hia protein provided herein protects in passive models of type a and type b infection, it is likely that it will also protect against type c disease due to sequence similarity between the type b and type c proteins.

The nucleotide and deduced amino acid sequences of the *hia* locus from strain 12 are shown in Figure 25. NTHi strain 12 does not produce Hia. However, part of the *hia* gene can be PCR amplified, there is

inconsistent positive reactivity of SB12 cell lysates with anti-rHia antibody, and there is reactivity with a DNA probe derived from the 3'-end of the strain 11 *hia* gene, on Southern blots. Analysis of the PCR amplified DNA, revealed a 1.8 kb fragment that contains 1 kb of the 3'-end of the upstream HI1732-related gene and 0.8 kb of the 3'-end of the *hia* gene.

PCR amplification using primers that would amplify across the putative junction of these two genes in strain 12, confirmed the genetic composition of the locus. Thus it would appear that strain 12 does not produce Hia because it has suffered a deletion of the 5'-end of the *hia* gene. Figure 27 shows a sequence comparison between the upstream orf of strain 12 and the Rd genome deduced HI1733 protein. Over the region of homology, the two proteins are 95% identical.

An alignment of the deduced Hia sequences from NTHi strains 33, 32, 29, K22, M4071, 11 and K9 and type c strain API compared with *H. influenzae* type b Hsf, the aidA-like (Hsf/Hia) HI1732 gene from the Rd genome, and the *M. catarrhalis* 200 kDa protein from strains 4223 and LES-1 is shown in Figure 28. There is a frame shift in the Rd genome sequence resulting in premature truncation of the HI1732 protein. Additional downstream sequence related to hia, is included here. The asterisks below the sequence indicate conserved residues. The N-terminal (approximately 50 residues) and C-terminal sequences (approximately 150 residues) are highly conserved amongst the *Haemophilus* strains, while some similarity is evident with the *M. catarrhalis* counterpart. Sequence analysis reveals that

there are two potential gene families of Hia proteins, one related to the prototype strain 11 and the other more closely related to strain 33. The strains 11 and K9 proteins appear to be more like the Hsf proteins from the type b, type c or type d *Haemophilus* strains while the strains 33, 32, 29, K22 and M4071 proteins appear to form a second family.

Example 15

This Example describes the construction of plasmid JB-2930-3 that contains a *T7 hia* gene cassette with a truncated S44 strain 11 *hia* gene, the *E. coli cer* gene, and the kanamycin antibiotic resistance gene, and expression of S44 Hia proteins.

PCR primers were designed to amplify the S44 Hia N-terminus of the NTHi strain 11 *hia* gene from the S44 amino acid to an internal *Sty* I site (Fig 29). An *Nde* I site was added at the 5'-end for cloning purposes and the fragment was amplified using plasmid DS-2242-1 as a template. The fragment was cloned into pCR II generating plasmid JB-2910-1-1. The construction scheme is shown in Figure 30. Plasmid JB-2910-1-1 was digested with *Nde* I and Sty I and the 5' PCR *hia* fragment isolated. Plasmid IA-46-5 containing the V38 hia gene was digested with *Nde* I and Sty I and the larger approximately 8.5 kb fragment purified. The two purified fragments were ligated together to produce plasmid JB-2917-1. This plasmid was then digested with *Nde* I and treated with calf intestinal phosphatase (CAP), and into it was cloned the T7 promoter from plasmid IA-46-5. The promoter was cut out using *Nde* I digestion of IA-46-5. The resulting plasmid, JB-2925-3,

was digested with *Bgl* II and *Bam* HI and the *hia* gene was isolated. This fragment was ligated into the *Bgl* II/CAP-treated plasmid BK-2-1-2 to produce plasmid JB-2930-3. This plasmid contains the T7 promoter S44 *hia* gene and *E. coli cer* gene and kanamycin resistance.

The recombinant S44 *hia* vector was transformed into *E. coli* BL21(DE3) for expression studies. The procedure for expression in *E. coli* was as described in Example 9. Figure 31 SDS-PAGE analysis of shows the expression of recombinant S44 *hia* from two different vectors, JB-2930-3 (described above) and pET vector IA-191-3-1. Plasmid IA-191-3-1 is identical to JB-2930-3 except it is a pET vector containing the $lacI^q$ repressor and, therefore, the amount of S44 *Hia* produced is less than the T7 S44 from JB-2930-3. The plasmid is shown, along with plasmid JB-2930-3, Figure 32. Figure 31 shows the S44 *Hia* as a doublet band (lane 3) at approximately 116 kDa. Upon further analysis using purified S44 *hia* from JB-2930-3, the lower band of the doublet was found to have a C-terminal truncation of 94 amino acids, while retaining the expected N-terminus. The purification process used for isolation of the truncated Hia was as described in Example 10.

SUMMARY OF THE DISCLOSURE

In summary of this disclosure, the present invention provides novel isolated and purified nucleic acid molecules encoding full-length and N-terminal truncated *Haemophilus influenzae* adhesin (Hia) proteins from *Haemophilus* which enable protective Hia proteins

to be produced recombinantly. Modifications are possible within the scope of this invention.

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TABLE 1

Protective effect of guinea pig anti-rHia (full-length) antiserum against type a or b *H. influenzae* in the infant rat model of bacteremia

Group (#)	Guinea pig serum	Anti-rHia antibody titers	No. bacteremic/ No. challenged	Mean cfu/ 100 µl blood
1	Anti-type a	nd	0/10*	0**
2	Anti-rHia	204,800	1/10*	0**
3	Preimmune	<100	7/10	88
Group (#)	Guinea pig serum	anti-rHia antibody titers	No. bacteremic/ No. challenged	Mean cfu/ 2.5 µl blood
4	Anti-MinnA	nd	0/10*	0**
5	Anti-rHia	204,800	1/10*	2**
6	Preimmune	<100	10/10	600

Five-day old infant rats were passively immunized s.c. with 0.1 ml of indicated guinea pig antiserum or preimmune serum. Twenty hours later, infant rats were challenged i.p. with either freshly grown *H. influenzae* type a strain ATCC 9006 (10^5 cfu, 0.1 ml) for groups #1 to 3; or with freshly grown Hib strain MinnA (240 cfu, 0.1 ml) for groups # 4 to 6. Infected animals are defined as >20 cfu recovered from 100 µl of blood for groups #1 to 3; or >30 cfu recovered from 2.5 µl of blood for groups # 4 to 6.

* Fisher exact test. Statistical significance compared to animals in group 3 or 6 was found ($P<0.05$).

** Student's unpaired *t* test. Statistical significance compared to animals in group 3 or 6 was found ($P<0.05$).

nd: not determined.

TABLE 2

Protective effect of guinea pig anti-V38 rHia (SB11) antiserum against type a or b *H. influenzae* in the infant rat model of bacteremia

Group (#)	Guinea pig serum	Anti-rHia antibody titers	No. bacteremic/ No. challenged	Mean cfu/ 20 µl blood
1	Anti-type a	nd	0/6*	0**
2	Anti-rHia	204,800	1/9*	5**
3	Preimmune	<100	5/8	165
Group (#)	Guinea pig serum	anti-rHia antibody titers	No. bacteremic/ No. challenged	Mean cfu/ 2 µl blood
4	Anti-MinnA	nd	0/6*	0**
5	Anti-rHia	204,800	1/9*	2**
6	Preimmune	<100	10/10	820

Five-day old infant rats were passively immunized s.c. with 0.1 ml of indicated guinea pig antiserum or preimmune serum. Twenty hours later, infant rats were challenged i.p. with either freshly grown *H. influenzae* type a strain ATCC 9006 (10^5 cfu, 0.1 ml) for groups #1 to 3; or with freshly grown Hib strain MinnA (190 cfu, 0.1 ml) for groups #4 to 6. Infected animals is defined as >20 cfu recovered from 20 µl of blood for groups #1 to 3; or >30 cfu recovered from 2 µl of blood for groups #4 to 6.

* Fisher exact test. Statistical significance compared to animals in group 3 or 6 was found ($P<0.05$)

** Student's unpaired *t* test. Statistical significance compared to animals in group 3 or 6 was found ($P<0.05$).

nd: Not determined.

CLAIMS

1. An isolated and purified nucleic acid molecule encoding a *Haemophilus influenzae* adhesin (Hia) protein of a strain of *Haemophilus influenzae* having:

(a) a DNA sequence selected from the group consisting of those shown in Figures 18, 20, 21, 22, 23, 24 and 25 (SEQ ID Nos: 23, 27, 29, 31, 33, 35, 37); or

(b) a DNA sequence encoding a *Haemophilus influenzae* adhesin (Hia) protein having an amino acid sequence selected from the group consisting of those shown in Figures 18, 20, 21, 22, 23, 24 and 25 (SEQ ID Nos: 24, 28, 30, 32, 34, 36, 38).

2. An isolated and purified nucleic acid molecule encoding an N-truncated *Haemophilus influenzae* adhesin (Hia) protein of a strain of *Haemophilus influenzae* which is amplifiable by a pair of nucleotides which are selected from the group consisting of:

SEQ ID No: 7 and SEQ ID No: 15
SEQ ID No: 9 and SEQ ID No: 15
SEQ ID No: 11 and SEQ ID No: 15
SEQ ID No: 13 and SEQ ID No: 15
SEQ ID No: 55 and SEQ ID No: 57

3. An isolated and purified nucleic acid encoding an N-truncated *Haemophilus influenzae* adhesin (Hia) protein of a strain of *Haemophilus influenzae* expressed as inclusion bodies, said N-truncated protein having the ability to bind to human epithelial cells.

4. The nucleic acid molecule of claim 3 which encodes a truncated Hia protein selected from the group consisting of the E21, T33, V38 and N52 truncations of *Haemophilus influenzae* strain 11 and the V38 truncation of *Haemophilus influenzae* strain 33.

5. A vector for transforming a host comprising the nucleic acid molecule of claim 1.

6. A vector for transforming a host comprising the nucleic acid molecule of any one of claims 2 to 4.

7. The vector of claim 5 or 6 which is a plasmid vector.

8. The vector of claim 7 wherein said plasmid vector has the identifying characteristics of a plasmid which is selected from the group consisting of:

DS-2008-2-3 as shown in Figure 1A
DS-2186-1-1 as shown in Figure 5A
DS-2201-1 as shown in Figure 5A
DS-2186-2-1 as shown in Figure 5A
DS-2168-2-6 as shown in Figure 5A
IA-191-3-1 as shown in Figure 32

9. A vector for transforming a host, comprising a nucleic acid molecule encoding a full-length *Haemophilus influenzae* adhesin (Hia) protein as claimed in claim 1 or N-truncated *Haemophilus influenzae* adhesin (Hia) protein as claimed in any one of claims 2 to 4 and a promoter operatively connected to said nucleic acid molecule for expression of said full-length or truncated Hia protein.

10. The vector of claim 9 further comprising the *cer* gene of *E. coli*.

11. The vector of claim 9 which is a plasmid vector.

12. The vector of claim 11 wherein said plasmid vector has the identifying characteristics of a plasmid vector which is selected from the group consisting of:

BK-96-2-11 as shown in Figure 6A
DS-2242-1 as shown in Figure 7A
DS-2242-2 as shown in Figure 7A
DS-2340-2-3 as shown in Figure 8A
DS-2447-2 as shown in Figure 9A
DS-2448-17 as shown in Figure 9B
JB-2930-3 as shown in Figure 32

13. A host cell transformed by a vector as claimed in claim 5, 6 or 9 and expressing a protective *Haemophilus influenzae* adhesin (Hia) protein of a non-typeable strain of *Haemophilus*.

14. The host cell of claim 13 which is a strain of *E. coli*.

15. A recombinant protective *Haemophilus influenzae* adhesin (Hia) protein of a strain of *Haemophilus influenzae* producible by the transformed *E. coli* of claim 14 or an immunogenic fragment thereof.

16. An immunogenic composition, comprising at least one immunologically-active component selected from the group consisting of:

(A) an isolated and purified nucleic acid molecule encoding a *Haemophilus influenzae* adhesin (Hia) protein of a strain of *Haemophilus influenzae* having:

(a) a DNA sequence selected from the group consisting of those shown in Figures 18, 20, 21, 22, 23, 24 and 25 (SEQ ID Nos: 23, 27, 29, 31, 33, 35, 37); or

(b) a DNA sequence encoding a *Haemophilus influenzae* adhesin (Hia) protein having an amino acid sequence selected from the group consisting of those shown in Figures 18, 20, 21, 22, 23, 24 and 25 (SEQ ID Nos: 24, 28, 30, 32, 34, 36, 38);

(B) an isolated and purified nucleic acid molecule encoding an N-truncated *Haemophilus influenzae* adhesin (Hia) protein of a strain of *Haemophilus influenzae* which is amplifiable by a pair of nucleotides which are selected from the group consisting of:

SEQ ID No: 7 and SEQ ID No: 15
SEQ ID No: 9 and SEQ ID No: 15
SEQ ID No: 11 and SEQ ID No: 15
SEQ ID No: 13 and SEQ ID No: 15
SEQ ID No: 55 and SEQ ID No: 57;

(C) an isolated and purified nucleic acid molecule encoding a truncated *Haemophilus influenzae* adhesin (Hia) protein of a strain of *Haemophilus influenzae* expressed as inclusion bodies, said N-truncated protein having the ability to bind to human epithelial cells; and

(D) a recombinant protective *Haemophilus influenzae* adhesin (Hia) protein of a strain of *Haemophilus influenzae* producible by a strain of *E. coli* transformed by an expression vector as claimed in claim 5, 6 or 9; and

a pharmaceutically-acceptable carrier therefor.

17. The immunogenic composition of claim 16 formulated as a vaccine for *in vivo* administration to protect against disease caused by *Haemophilus*.

18. The immunogenic composition of claim 16 in combination with a targeting molecule for delivery to specific cells of the immune system or to mucosal surfaces.

19. The immunogenic composition of claim 16 formulated as a microparticle, capsule or liposome preparation.

20. The immunogenic composition of claim 16 further comprising an adjuvant.

21. A method for inducing protection against disease caused by *Haemophilus*, comprising administering to a susceptible host an effective amount of the immunogenic composition of claim 16.

22. The method of claim 21 wherein the susceptible host is a human.

23. A method for the production of a protective *Haemophilus influenzae* adhesin (Hia) protein of a non-typeable strain of *Haemophilus influenzae*, which comprises:

transforming a host with a vector as claimed in claim 6,

growing the host cell to express the encoded truncated Hia, and

isolating and purifying the expressed Hia protein.

24. The method of claim 23 wherein the host cell is *E. coli*.

25. The method of claim 23 wherein said encoded truncated Hia is expressed in inclusion bodies.

26. The method of claim 25 wherein said isolation and purification of the expressed Hia is effected by:

disrupting the grown transformed cells to produce a supernatant and the inclusion bodies,

solubilizing the inclusion bodies to produce a solution of the recombinant Hia,

chromatographically purifying the solution of recombinant Hia free from cell debris, and

isolating the purified recombinant Hia protein.

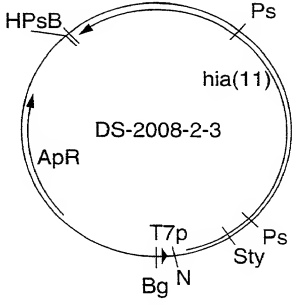
27. The method of claim 23 wherein said non-typeable strain of *Haemophilus* is selected from the group consisting of strains 11, 33, 32, 29, M4071, K9, K22 and 12.

28. The method of claim 23 wherein said vector includes the T7 promoter and said *E. coli* is cultured in the presence of an inducing amount of lactose.

29. A pair of nucleotide sequences capable of amplifying and generating a nucleic acid molecule encoding an N-truncated *Haemophilus influenzae* adhesin (Hia) protein of a strain of *Haemophilus influenzae*, which pair of nucleotides is selected from the group consisting of:

SEQ ID No: 7 and SEQ ID No: 15
SEQ ID No: 9 and SEQ ID No: 15
SEQ ID No: 11 and SEQ ID No: 15
SEQ ID No: 13 and SEQ ID No: 15
SEQ ID No: 55 and SEQ ID No: 57

Restriction map of DS-2008-2-3, pT7 hia (11).



pT7 hia (11)

FIG.1A

FIG.1B

Oligonucleotides used to PCR amplify the full-length strain 11 *hia* gene for expression studies.

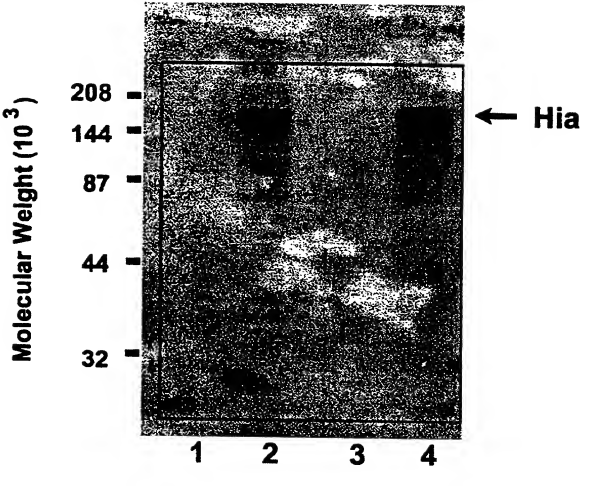
sense

```
        EcoR I Nde I
          ↓      ↓
                  M  N  K  I  F  N  V  I  W  N     P                          SEQ ID NO:2
5'   GCGAATTCATATGAACAAAATTTTTAACGTTATTTGGAAT     3'          5038.SL         SEQ ID NO:1
```

antisense

```
         K  T  G  V  A  A  G  V  G  Y  Q  W  *  *                                      SEQ ID NO:5
5'     AAAACAGGCGTTGCAGCAGGTGTTGGTTACCAGTGGTAATAG                      3'               SEQ ID NO:4
3'     TTTTGTCCGCAACGTCGTCCACAACCAATGGTCACCATTATCTTAAGGCCTAGGCG        5'    5039.SL    SEQ ID NO:3
                                                       ↑     ↑
                                                    EcoR I BamH I
```

FIG.2



Construction of DS-2092-1 and DS-2092-40,
plasmids containing tandem T7 hia (11) genes.

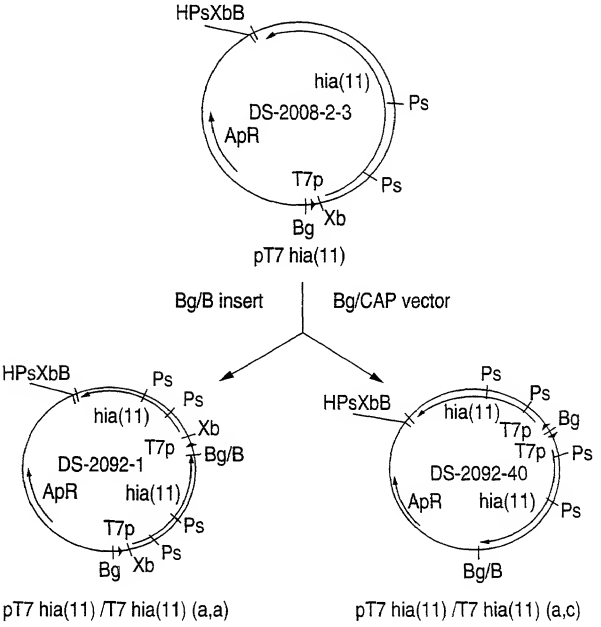


FIG.3

FIG.4

Sites for N-terminal truncations of rHia proteins.

MNKIFNVIWNVVIQTWVVVSE[21]LITKTHTTKCASA[33]TVAVAV[38]LATLLSATVEANAN[52]TPVTNKLFKAYGD (SEQ ID NO.6)

6/204

Construction of plasmids expressing truncated hia (11) genes.

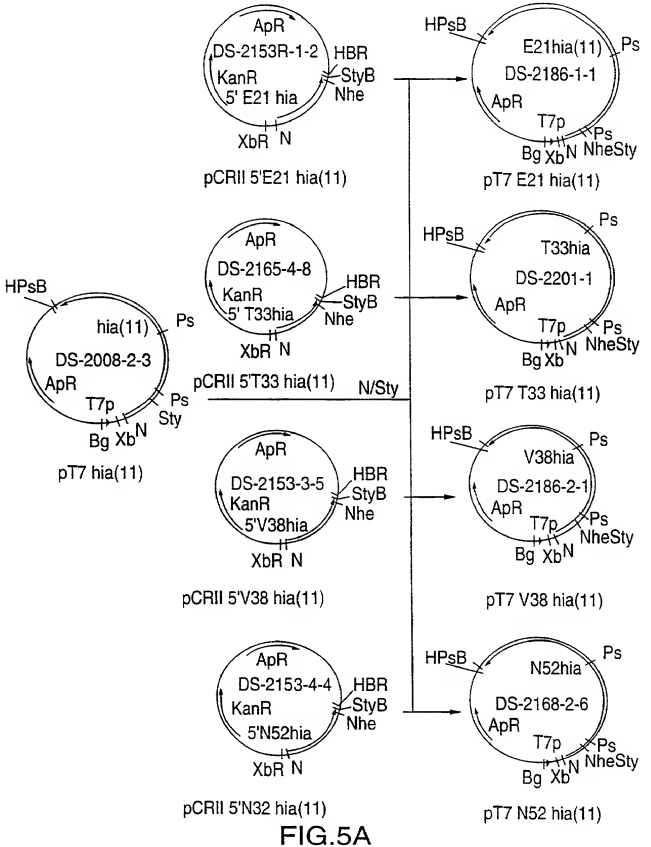


FIG.5A

FIG.5B

Oligonucleotidé primers to PCR amplify truncated strain 11 *hia* genes.

E21

EcoR I Nde I

	M E L T R T H T K C A			SEQ ID NO: 8
5′	GGGAATTCATATGGAACTCACTCGCACCCACACCAAATGGGCC	3′	5524.SL	SEQ ID NO: 7

T33

	M T V A V A V L A T L			SEQ ID NO:10
5′	GGGAATTCATATGACCGTGGCGGTTGCCGTATTGGCAACCCTG	3′	5525.SL	SEQ ID NO: 9

V38

	M V L A T L L S A T			SEQ ID NO:12
5′	GGGAATTCATATGGTATTGGCAACCCTGTTGTCCGCAACG	3′	5526.SL	SEQ ID NO:11

09/936,369
PCT/CA00/00289

FIG.5B'

N52

M N T P V T N K L K A

5' GGGAATTCATATGAATACTCCGTTACGAATAAGTTGAAGGCT 3' 5527.SL SEQ ID NO:13

SEQ ID NO:14

antisense

H T I T F A L A K D L G

5' CACACCATTACCTTTGCGCTAGCGAAAGACCTTCGTGG 3' SEQ ID NO:16

3' GTGTGGTAATGGAAACGCGATCGCTTTCTGGAACCACCCTAGCGC 5' 5528.SL SEQ ID NO:15

SEQ ID NO:17

Nhe I Sty I BamH I

Construction of BK-96-2-11,
a plasmid containing T7 V38 hia(11) and cer.

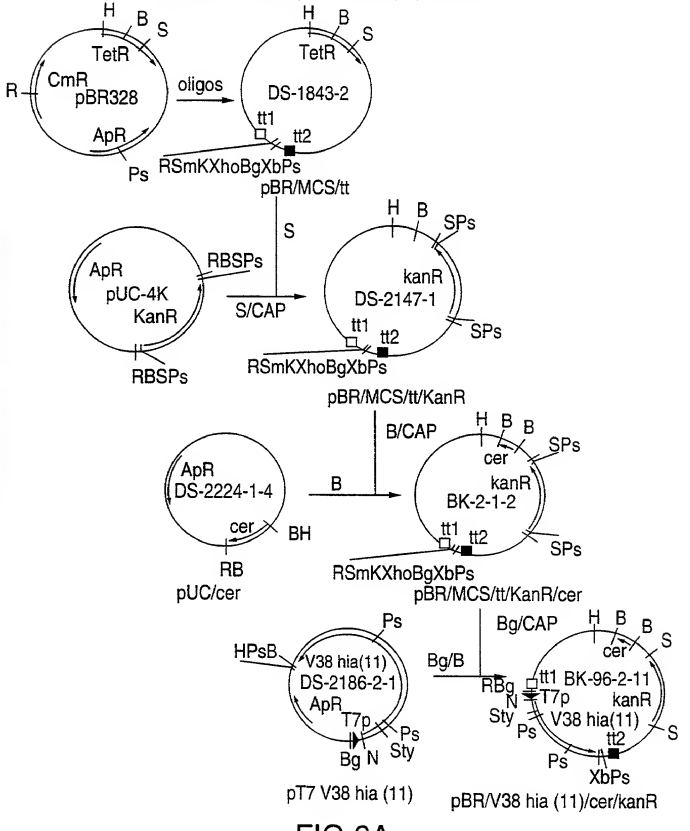


FIG.6A

FIG.6B

Oligonucleotides used to generate the multiple cloning site and transcription terminators for the expression plasmids

```
                                          R      Sm
"R"          trpA terminator              ↓      ↓      KXho   Bg  Xb     ...
AATTGCAGCCCGCCTAATGAGCGGGCTTTTTTGAATTCCCGGGTA   ↓↓     ↓    ↓       ...
                                                  CCTCGAGATCTCTAGAC...
    CGTCGGGCGGATTACTCGCCCGAAAAAACTTAAGGGCCCATGGAGCTCTAGAG
                                                              ATCTG...

                                       ...   Ps
                                       ...   ↓          T7 gene 10 terminator
                                       ...TGCAGATATAGTTCCTCCTTTCAGCAAAAAACCCCTCAA

                                       ...ACGTCTATATCAAGGAGGAAAGTCGTTTTTTGGGGAGTTCTGGGCAAATC

                                                             "Ps"
GACCCGTTTAGAGGCCCCAAGGGGTTATGCTAGTTATTGCTCAGCGGTGGCAGCAGCGTGCA       SEQ ID NO:50
            TCCGGGGTTCCCCAATACGATCAATAACGAGTCGCCACCGTCGTCGC          SEQ ID NO:51
```

11/204

Construction of DS-2242-1 and DS-242-2, plasmids containing T7 hia (33) and cer.

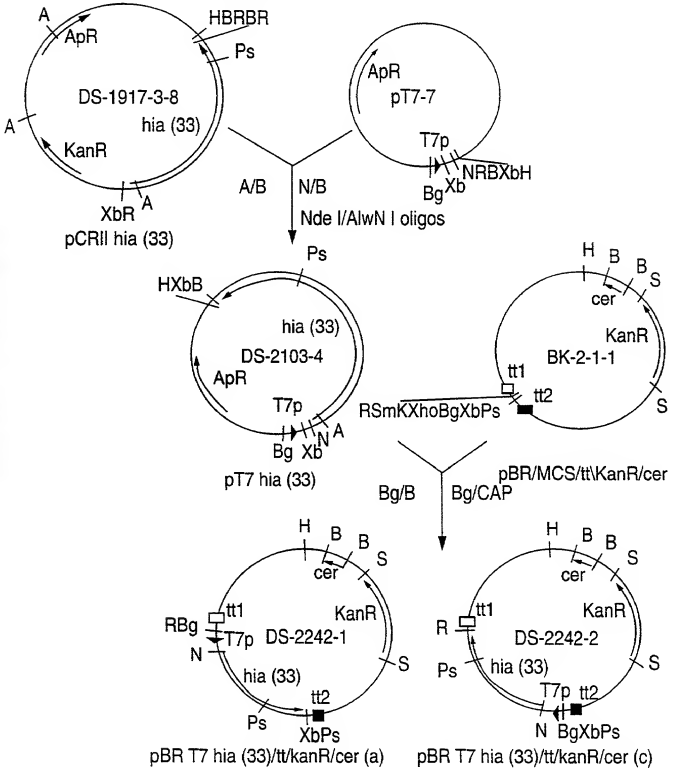


FIG.7A

FIG.7B

Oligonucleotides used to generate the 5'-end of the strain 33 *hia* gene for expression studies.

```
Nde I
↓
  M  N  K  I  F  N  V  I  W  N  V  M  T  Q  T  W  A  V  V  S  E  L  T  R  A  H  T  K...
TATGAACAAAATTTTTAACGTTATTTGGAATGTTATGACTCAAACTTGGGCTGTCG
                                                    TATCTGAACTCACTCGCGCCCACACCA...
ACTTGTTTTAAAAATTGCAATAAACCTTACAATACTGAGTTT
                                                    GAACCCGACAGCATAGACTTGAGTGAGCGCGGGTGTGGT...
                                                                                    ...
                                                                  ... R  A  S  A  T  V  A  A    SEQ ID NO:54
                                                    ...AACGTGCCTCCCCAACCGTGCCAGCCG SEQ ID NO:52
                                                    ...TTGCACCGAGGCGTTGGCACCGTC    SEQ ID NO:53
                                                                                    ↓
                                                                                    ...
                                                                                    AlwN I
```

Construction of DS-2340-2-3,
a plasmid containing T7 V38 hia (33) and cer.

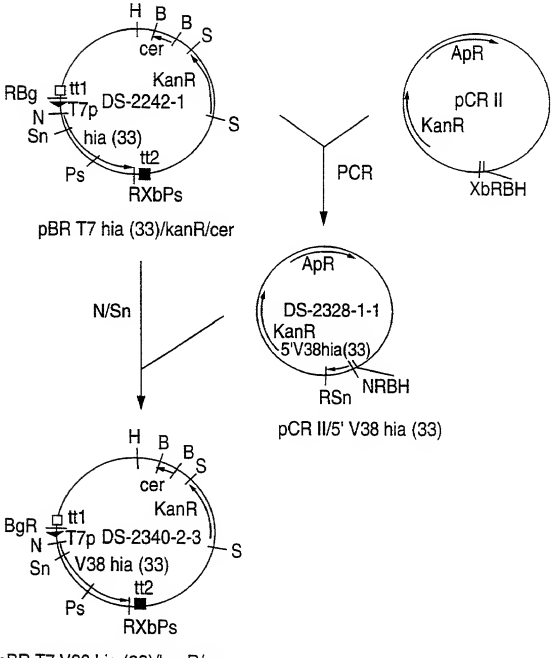


FIG.8A

FIG.8B

Oligonucleotides used to PCR amplify the strain 33 hia gene from the V38 codon to the SnaB I site.

sense

Nde I

M V L A T V L S A T

5′ GGGAATTCATATGGTATTGGCGACCGTATTGTCTGCAACG 3′ 6286.SL SEQ ID NO:60

SEQ ID NO:61

antisense

SnaB I

D E T T A T V G N L R K L

5′ GACGAAACCACCGCAACCGTAGGCAATTTACGTAAATTGAAGCTTCG 3′ SEQ ID NO:19

3′ CTGCTTTGGTGGCGTTGGCATCCGTTAAATGCATTTAACTTCGAAGC 5′ 6287.SL SEQ ID NO:18

SEQ ID NO:20

Construction of DS-2447-2,
a plasmid containing tandem T7 V38 hia (11) cassettes and cer.

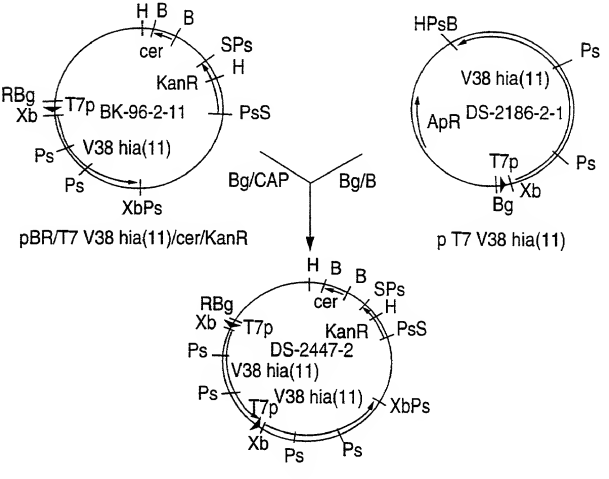


FIG.9A

Construction of DS-2448-17,
a plasmid containing tandem T7 V38 hia(33) cassettes and cer.

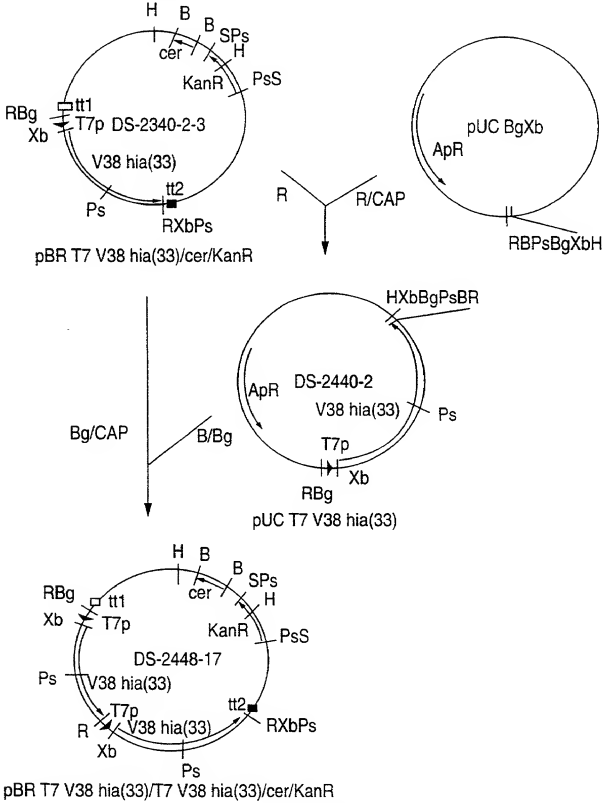
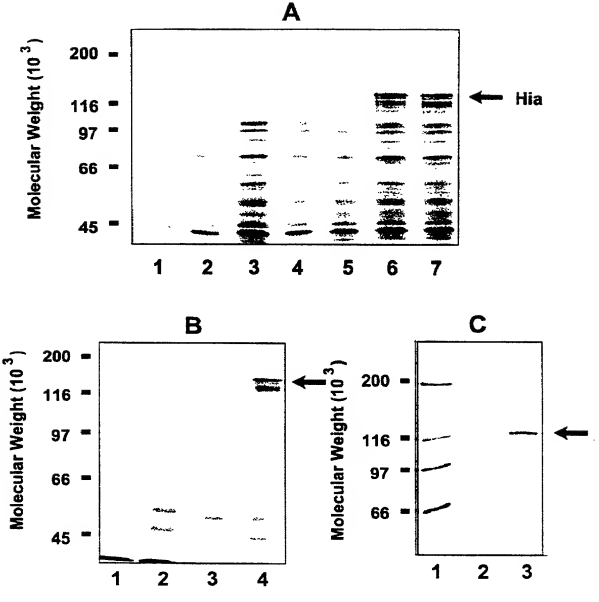


FIG.9B

FIG.10


A
Molecular Weight (10^3)
200
116
97
66
45
Hia
1 2 3 4 5 6 7
B
Molecular Weight (10^3)
200
116
97
66
45
1 2 3 4
C
Molecular Weight (10^3)
200
116
97
66
1 2 3

18/204

Purification of rHia Proteins from E. coli

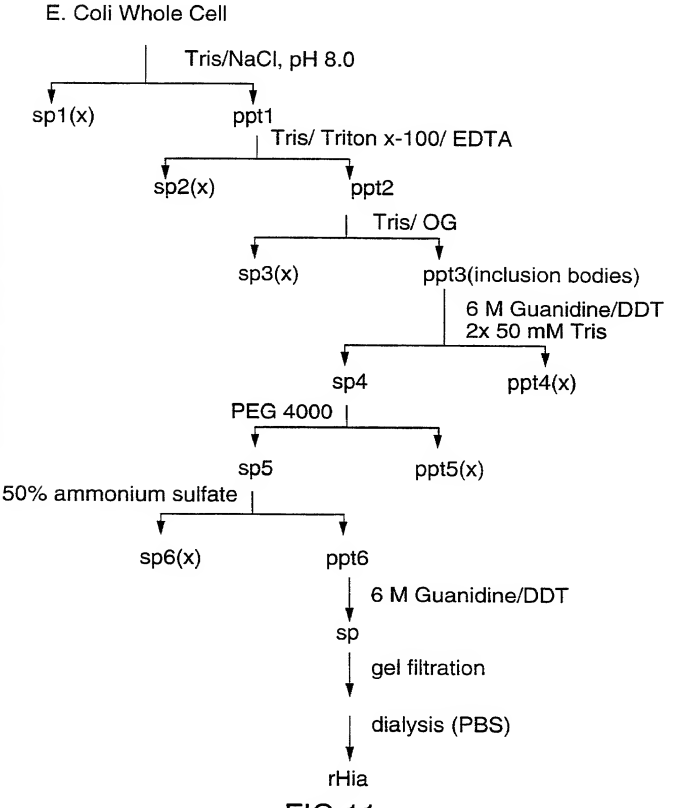
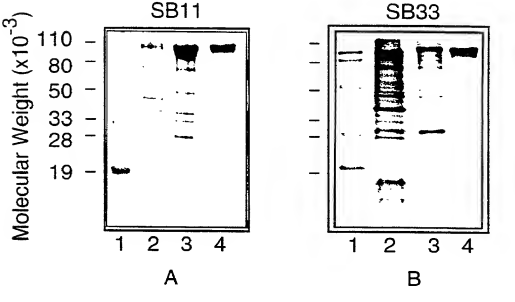


FIG.11

Purification of rHia (V38) from E. coli



1. Prestained molecular weight markers
2. E. coli whole cell lysate
3. Crude extract
4. Purified rHia protein

FIG.12

20/204

The Stability of rHia (V38/SB11)

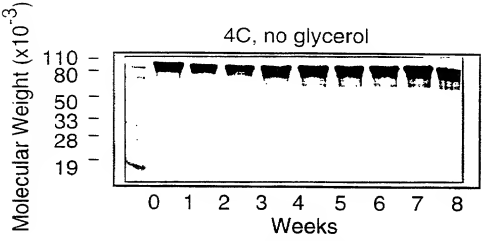


FIG.13A

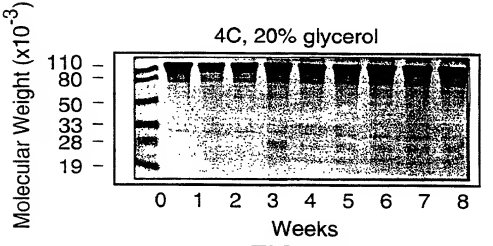


FIG.13B

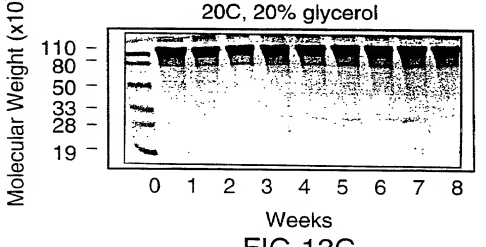


FIG.13C

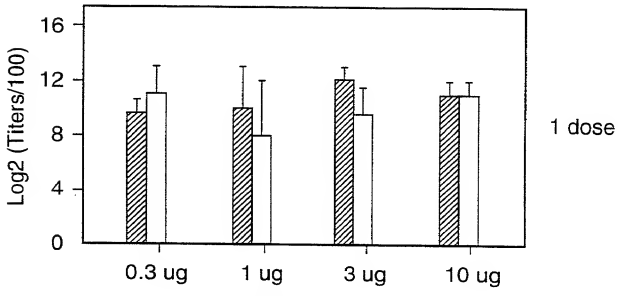


FIG.14A

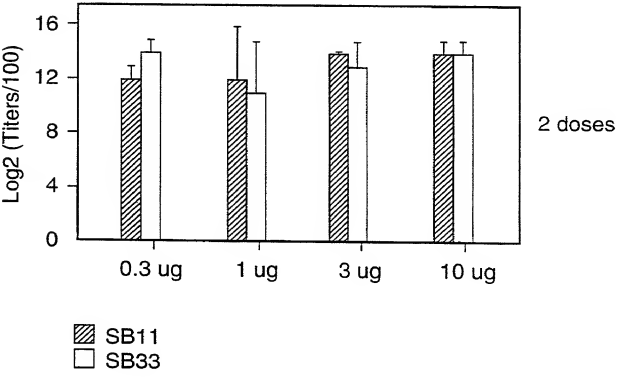


FIG.14B

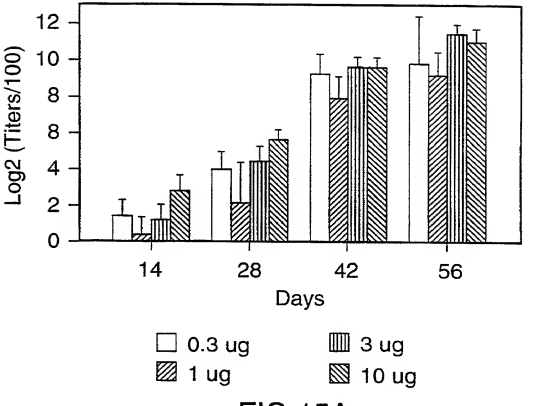

Anti-V38 rHia (SB11) Antibody Titers in BALB/c Mice
Log2 (Titers/100)
12
10
8
8
4
2
0
14
28
42
56
Days
0.3 ug
3 ug
1 ug
10 ug

FIG.15A

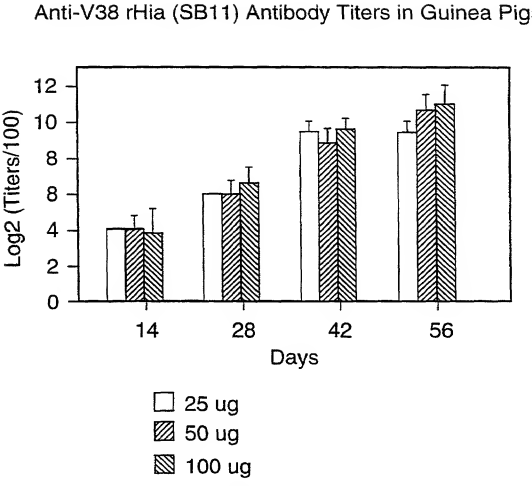

Anti-V38 rHia (SB11) Antibody Titers in Guinea Pigs
Log2 (Titers/100)
12
10
8
8
4
2
0
14
28
42
56
Days
25 ug
50 ug
100 ug

FIG.15B

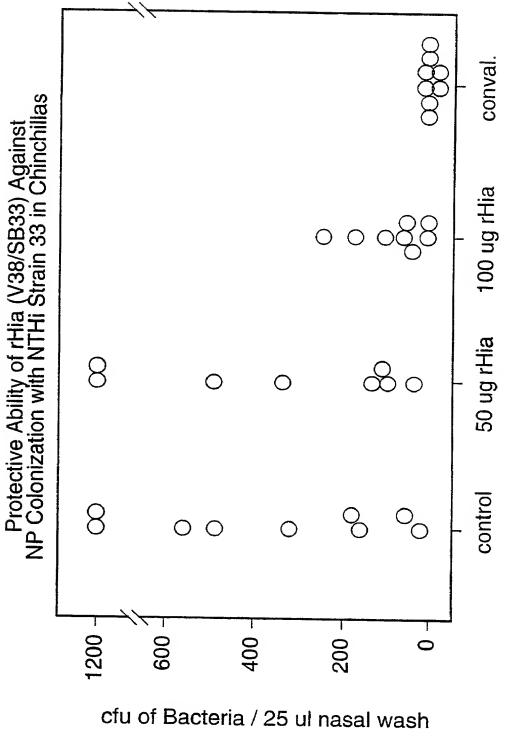

Protective Ability of rHia (V38/SB33) Against
NP Colonization with NTHi Strain 33 in Chinchillas
1200
600
400
200
0
cfu of Bacteria / 25 ul nasal wash
control
50 ug rHia
100 ug rHia
conval.

FIG.16

FIG.17

Oligonucleotides used to PCR amplify additional *hia* genes.

sense

```
                    M  N  K  I  F  N  V                                    SEQ ID NO:22
5'  TTAAATATAAGGTAAATAAAAATGAACAAAATTTTTAACGTT   3'        5040.SL        SEQ ID NO:21
```

antisense

```
       K  T  G  V  A  A  G  V  G  Y  Q  W  *  *                           SEQ ID NO:5
5'  AAAACAGGCGTTGCAGCAGGTGTTGGTTACCAGTGGTAATAG                  3'         SEQ ID NO:4
3'  TTTTGTCCGCAACGTCGTCCACAACCAATGGTCACCATTATCTTAAGGCCTAGGCG    5'  5039.SL SEQ ID NO:3
                                  ↑     ↑
                              EcoR I  BamH I
```

FIG.18A

NTHi strain 33 Hia

```
                                    MET   ASN   LYS...
G A A T T C G G C T T A A A T A A A A A T G A A C A A ...
          10                  20                  ...
                         ...  ILE   PHE   ASN   VAL   ILE   TRP   ASN   VAL   MET   THR   GLN
                         ...A A T T T T A A C G T T A T T T G G A A T G T T A T G A C T C A
                         ...   30                  40                  50                  60

   THR   TRP   ALA   VAL   VAL   SER   GLU   LEU   THR...
A A C T T G G G C T G T C G T A T C T T G A A C T C A C ...
                70                  80                  ...
                         ...   ARG   ALA   HIS   THR   LYS   ARG   ALA   SER   ALA   THR   VAL
                         ...T C G C G C C C A C A C C A A A C G T G C C T C C G C A A C C G T
                         ...   90                  100                 110                 120

   ALA   ALA   ALA   VAL   LEU   ALA   THR   VAL   LEU...
G G C A G C C G C T G T A T T G G C G A C C G T A T T ...
          130                 140                 ...
                         ...   SER   ALA   THR   VAL   GLN   ALA   SER   ALA   GLY   SER   THR
                         ...G T C T G C A A C G G T T C A G G C G A G T G C A G G C A G T A C
                         ...   150                 160                 170                 180

   THR   GLY   THR   ASN   SER   LEU   ASN   VAL   TYR...
G A C A G G T A C A A A T A G T T T G A A T G T T T A ...
          190                 200                 ...
```

FIG.18B

```
                ...  GLY  LYS  ASN  ASN  SER  ASN  PHE  ASN  SER  ALA  ASN
                ...T G G A A A G A A T A A T T C G A A T T T C A A T T C A G C C A A
                ...  210                  220                  230                  240

  ASN  SER  ILE  ALA  ASP  LEU  ASN  LYS  GLN...
T A A T T C A A T T A G C A G A T T T A A A T T A A A C A ...
                250                  260                  ...

                ...  ASN  ASP  SER  VAL  TYR  ASP  GLY  LEU  LEU  ASN  LEU
                ...A A A T G A T A G T G T T T A C G A T G G T T T A T T A A A T C T
                ...  270                  280                  290                  300

  ASN  GLU  LYS  GLY  THR  ASP  LYS  SER  LYS...
G A A T G A A A A A G G T A C G G A T A A G T C A A A ...
                310                  320                  ...

                ...  PHE  LEU  VAL  ALA  ASP  GLU  THR  THR  ALA  THR  VAL
                ...A T T C C T G G T T G C T G A C G A A A C C A C C G C A A C C G T
                ...  330                  340                  350                  360

  GLY  ASN  LEU  ARG  LYS  LEU  GLY  TRP  VAL...
A G G C A A T T T A C G T A A A T T G G G G T T G G G T ...
                370                  380                  ...

                ...  VAL  SER  THR  LYS  ASN  SER  THR  LYS  GLU  GLU  SER
                ...A G T A T C A A C C A A A A A C A G T A C G A A A G A A G A A A G
                ...  390                  400                  410                  420
```

FIG.18C

```
     ASN  GLN  VAL  LYS  GLN  ALA  ASP  GLU  VAL...
C A A T C A A G T C A A A A C A G G C G G A T G A A G T ...
                430                 440                 ...

                ...  LEU  PHE  GLU  GLY  LYS  ASP  GLY  VAL  THR  VAL  THR
                ...G T T G T T T G A A G G C A A A G A C G G T G T A A C G G T T A C
                ...  450                 460                 470                 480

     SER  LYS  SER  GLU  ASN  GLY  LYS  HIS  THR...
T T C C A A A T C T G A A A A C G G C A A A C A C A C ...
                490                 500                 ...

                ...  VAL  THR  PHE  ALA  LEU  ALA  ASN  ASP  LEU  ASN  VAL
                ...C G T T A C T T T T G C C C T T G C G A A T G A C C T T A A T G T
                ...  510                 520                 530                 540

     LYS  ASN  ALA  THR  VAL  SER  ASP  LYS  LEU...
A A A A A A C G C A A C C G T T A G C G A T A A A T T ...
                550                 560                 ...

                ...  SER  LEU  GLY  ALA  ASN  GLY  LYS  LYS  VAL  ASP  ILE
                ...A T C G C T T G G T G C A A A C G G C A A G A A A G T C G A T A T
                ...  570                 580                 590                 600

     THR  SER  ASP  ALA  ASN  GLY  LEU  LYS  PHE...
T A C C A G T G A T G C A A A C G G C T T G A A A T T ...
                610                 620                 ...
```

FIG.18D

```
...  ALA LYS GLN GLY THR ASN GLY GLN ASN GLY ASN
...T G C G A A A C A G G G T A C G A A T G G T C A A A A C G G T A A
...  630                640                650                660

VAL HIS LEU ASN GLY ILE ALA SER THR...
T G T T C A C T T A A A C G G T A T T G C T T C G A C ...
              670                680                ...
...  LEU ASP ASP PRO ARG VAL GLY GLY LYS THR ALA
...T T T A G A T G A T C C T C G T G T G G G T G G A A A A A C A G C
...  690                700                710                720

HIS LEU THR LYS GLU ILE SER ASP THR...
A C A C C T T A C A A A A G A A A T C A G C G A T A C ...
              730                740                ...
...  GLU ARG ASN ARG ALA ALA SER VAL GLY ASP VAL
...A G A A C G T A A C C G T G C T G C G A G C G T G G G C G A T G T
...  750                760                770                780

LEU ASN ALA GLY TRP ASN ILE ARG GLY...
A T T G A A T G C G G G T T G G A A T A T T C G T G G ...
              790                800                ...
...  ALA LYS THR ILE GLY GLY THR VAL ASP ASN VAL
...C G C A A A A A C G A T T G G C G G T A C A G T G G A T A A T G T
...  810                820                830                840
```

FIG.18E

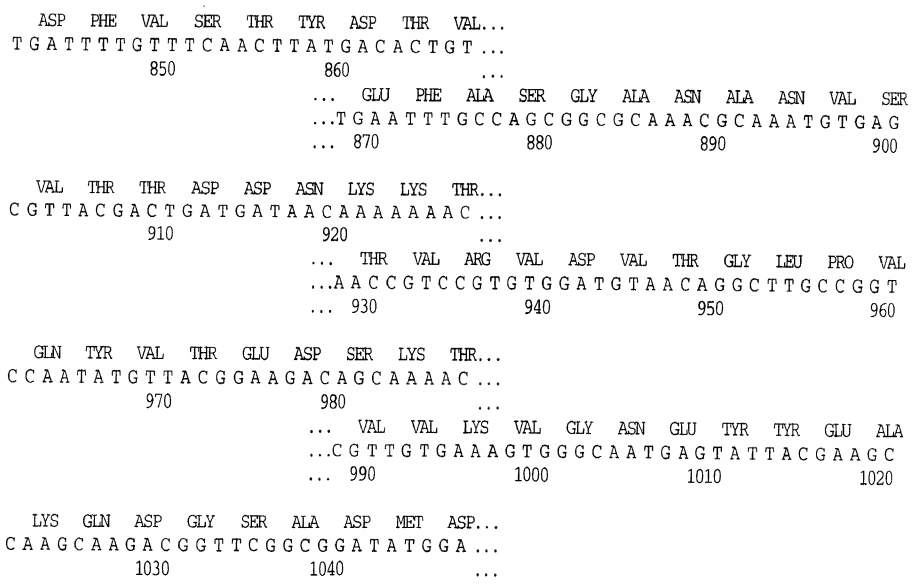


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FIG.18F

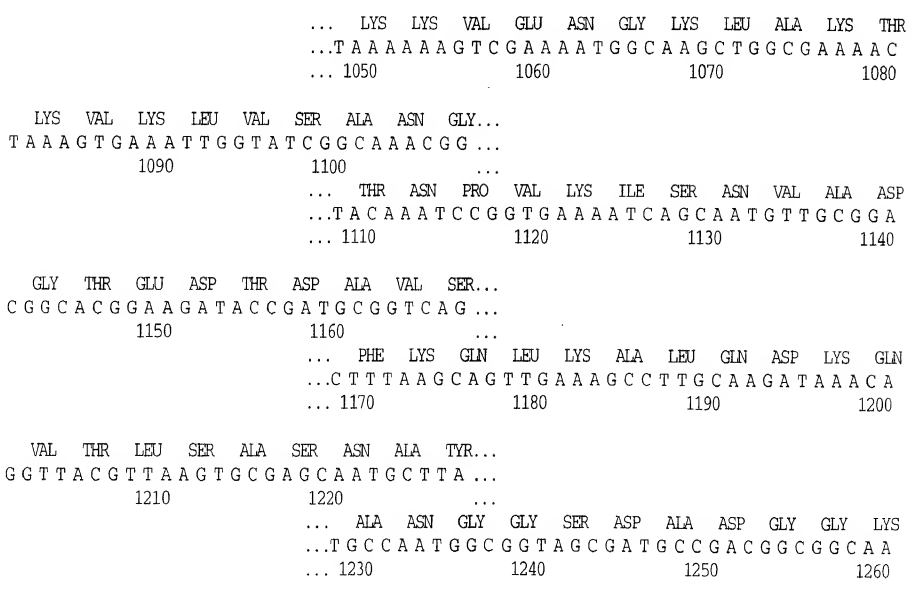


FIG.18G

```
   ALA  THR  GLN  THR  LEU  GLY  ASN  ASP  LEU...
GGCAACCTCAAACTTTAGGCAATGATTT...
          1270      1280      ...
...  ASN  PHE  LYS  PHE  LYS  SER  THR  ASP  SER  GLU  LEU
...GAATTTTAAATTTAAATCCACAGACAGCGAGTT
... 1290      1300      1310      1320

   LEU  ASN  ILE  LYS  ALA  ALA  GLY  ASP  THR...
GTTGAACATCAAAGCAGGTGACAC ...
          1330      1340      ...
...  VAL  THR  PHE  THR  PRO  LYS  LYS  GLY  SER  VAL  GLN
...GGTTACCTTTACGCCGAAAAAAGGTTCGGTGCA
... 1350      1360      1370      1380

   VAL  GLY  ASP  ASP  GLY  LYS  ALA  THR  ILE...
GGTTGGCGATGATGGTAAGGCTACGAT ...
          1390      1400      ...
...  GLN  ASP  GLY  ALA  LYS  THR  THR  THR  GLY  LEU  VAL
...TCAAGACGGCGCGAAAACAACTACCGGTTGGT
... 1410      1420      1430      1440

   GLU  ALA  SER  GLU  LEU  VAL  ASP  SER  LEU...
TGAGGCTTCTGAATTGGTTGACAGCCT ...
          1450      1460      ...
```

FIG.18H

```
                ...   ASN  LYS  LEU  GLY  TRP  LYS  VAL  GLY  VAL  GLY  LYS
                ...G A A C A A A T T G G G C T G G A A A G T G G G C G T T G G T A A
                ... 1470                 1480                 1490                 1500

      ASP  GLY  THR  GLY  ALA  THR  ASP  GLY  THR...
A G A C G G C A C A G G A G C G A C C G A T G G C A C ...
                1510                 1520                 ...

                ...   HIS  THR  ASP  THR  LEU  VAL  LYS  SER  GLY  ASP  LYS
                ...G C A T A C C G A C A C T T T A G T G A A G T C G G G C G A T A A
                ... 1530                 1540                 1550                 1560

      VAL  THR  LEU  LYS  ALA  GLY  ASP  ASN  LEU...
A G T A A C T T T G A A A G C C G G C G A T A A T C T ...
                1570                 1580                 ...

                ...   LYS  VAL  LYS  GLN  GLU  GLY  THR  ASN  PHE  THR  TYR
                ...G A A G G T C A A A A C A A G A G G G T A C A A A C T T C A C T T A
                ... 1590                 1600                 1610                 1620

      VAL  LEU  ARG  ASP  GLU  LEU  THR  GLY  VAL...
C G T G C T C A G A G A T G A A T T G A C G G G C G T ...
                1630                 1640                 ...

                ...   LYS  SER  VAL  GLU  PHE  LYS  ASP  THR  GLU  ASN  GLY
                ...A A A G A G C G T G G A G T T T A A A G A C A C G G A G A A T G G
                ... 1650                 1660                 1670                 1680
```

FIG.18I

```
 ALA  ASN  GLY  ALA  SER  THR  LYS  ILE  THR...
TGCAAACGGTGCAAGCACGAAGATTAC...
        1690      1700          ...
                    ...  LYS  ASP  GLY  LEU  THR  ILE  THR  PRO  ALA  ASN  ASP
                    ...CAAAGACGGCTTGACCATTACGCCGGCAAACGA
                    ... 1710      1720      1730      1740

 ALA  ASN  GLY  ALA  ALA  ALA  THR  ASP  ALA...
TGCGAATGGTGCGGCGGCGACTGATGC...
        1750      1760          ...
                    ...  ASP  LYS  ILE  LYS  VAL  ALA  SER  ASP  GLY  ILE  SER
                    ...TGACAAGATTAAAGTGGCTTCAGACGGCATTAG
                    ... 1770      1780      1790      1800

 ALA  GLY  ASN  LYS  ALA  VAL  LYS  ASN  VAL...
TGCGGGTAATAAAGCAGTTAAAAACGT...
        1810      1820          ...
                    ...  VAL  SER  GLY  LEU  LYS  LYS  PHE  GLY  ASP  ALA  ASN
                    ...TGTGAGCGGACTGAAGAAATTTGGTGATGCGAA
                    ... 1830      1840      1850      1860

 PHE  ASN  PRO  LEU  THR  SER  SER  ALA  ASP...
TTTCAATCCGCTGACTAGCTCAGCCGA...
        1870      1880          ...
```

FIG.18J

```
                        ...  ASN  LEU  THR  LYS  GLN  TYR  ASP  ASN  ALA  TYR  LYS
                        ...C A A C T T A A C G A A A C A A T A T G A C A A T G C C T A T A A
                        ... 1890            1900            1910            1920

 GLY  LEU  THR  ASN  LEU  ASP  GLU  LYS  SER...
A G G C T T G A C C A A T C T G G A T G A A A A A A G ...
           1930            1940             ...
                        ...  LYS  GLY  LYS  GLN  THR  PRO  THR  VAL  ALA  ASP  ASN
                        ...T A A A G G C A A G C A A A C T C C G A C C G T T G C T G A C A A
                        ... 1950            1960            1970            1980

 THR  ALA  ALA  THR  VAL  GLY  ASP  LEU  ARG...
T A C C G C T G C A A C C G T G G G C G A T T T G C G ...
           1990            2000             ...
                        ...  GLY  LEU  GLY  TRP  VAL  ILE  SER  ALA  ASP  LYS  THR
                        ...C G G T T T G G G C T G G G T C A T T T C T G C A G A C A A A A C
                        ... 2010            2020            2030            2040

 THR  GLY  GLU  SER  LYS  GLU  TYR  SER  ALA...
C A C A G G C G A G T C A A A G G A A T A T A G C G C ...
           2050            2060             ...
                        ...  GLN  VAL  ARG  ASN  ALA  ASN  GLU  VAL  LYS  PHE  LYS
                        ...G C A A G T G C G T A A C G C C A A T G A A G T G A A A T T C A A
                        ... 2070            2080            2090            2100
```

FIG.18K

```
    SER  GLY  ASN  GLY  ILE  ASN  VAL  SER  GLY...
G A G C G G C A A C G G T A T C A A T G T T T C C G G ...
                2110                              ...
                  ...  LYS  THR  LEU  ASP  ASN  GLY  THR  ARG  GLU  ILE  THR
                  ...T A A A A C A T T G G A T A A C G G T A C G C G C G A A A T T A C
                  ... 2130                   2140                   2150        2160

    PHE  GLU  LEU  ALA  LYS  ASP  GLU  ASN  ALA...
TT T T G A A T T G G C T A A A G A C G A A A A T G C ...
                2170                              ...
                  ...  ILE  ALA  PHE  GLY  SER  GLY  SER  LYS  ALA  LEU  ARG
                  ...C A T T G C T T T C G G T T C T G G C T C A A A G C C T T G C G
                  ... 2190                   2200                   2210        2220

    ASP  ASN  THR  VAL  ALA  ILE  GLY  THR  GLY...
C G A T A A C A C G G T G G C G A T T G G T A C G G G ...
                2230                              ...
                  ...  ASN  VAL  VAL  ASN  ALA  GLU  LYS  SER  GLY  ALA  PHE
                  ...C A A C G T T G T G A A T G C G G A A A A A T C T G G T G C A T T
                  ... 2250                   2260                   2270        2280

    GLY  ASP  PRO  ASN  TYR  ILE  GLU  ASP  LYS...
C G G C G A T C C G A A C T A C A T C G A A G A T A A ...
                2290                              ...
                                  2300
```

FIG.18L

```
                                ...  ALA  GLY  GLY  SER  TYR  ALA  PHE  GLY  ASN  ASP  ASN
                                ...AGCCGGTGGCAGCTACGCTTTCGGTAACGATAA
                                ... 2310          2320          2330          2340

  ARG  ILE  THR  SER  LYS  ASN  THR  PHE  VAL...
CCGTATTACTTCTAAAAACACTTTTGT...
          2350          2360          ...
                                ...  LEU  GLY  ASN  GLY  VAL  ASN  ALA  LYS  TYR  LYS  ALA
                                ...GTTGGGTAATGGAGTTAATGCGAAATATAAAGC
                                ... 2370          2380          2390          2400

  ASN  GLY  ASP  VAL  ASP  THR  GLU  THR  VAL...
CAATGGAGATGTTGATACGGAAACCGT...
          2410          2420          ...
                                ...  THR  VAL  LYS  ASP  LYS  ASP  GLY  LYS  GLU  THR  THR
                                ...AACTGTTAAGGACAAAGACGGTAAAGAGACTAC
                                ... 2430          2440          2450          2460

  VAL  THR  VAL  PRO  LYS  ALA  LEU  GLY  ALA...
CGTTACTGTTCCTAAAGCGTTAGGGGC...
          2470          2480          ...
                                ...  THR  VAL  GLU  ASN  SER  VAL  TYR  LEU  GLY  ASN  LYS
                                ...TACGGTTGAAAACTCCGTTTATTTGGGTAATAA
                                ... 2490          2500          2510          2520
```

09/936362

FIG.18M

```
SER  THR  ALA  THR  LYS  ASP  LYS  GLY  LYS...
A T C G A C T G C G A C A A A A G A T A A G G T A A ...
          2530           2540            ...
                         ...  ASN  LEU  LYS  SER  ASP  GLY  THR  ALA  GLY  ASN  THR
                         ...A A A T C T G A A A T C T G A T G G T A C G G C G G T A A C A C
                         ... 2550           2560           2570           2580

THR  THR  ALA  GLY  THR  THR  GLY  THR  VAL...
T A C A A C T G C T G G T A C A A C G G G T A C G G T ...
          2590           2600            ...
                         ...  ASN  GLY  PHE  ALA  GLY  ALA  THR  ALA  HIS  GLY  ALA
                         ...A A A C G G C T T T G C C G G T G C A A C G G C G C A C G G T G C
                         ... 2610           2620           2630           2640

VAL  SER  VAL  GLY  ALA  SER  GLY  GLU  GLU...
G G T T T C T G T C G G C G C A A G C G G C G A A G A ...
          2650           2660            ...
                         ...  ARG  ARG  ILE  GLN  ASN  VAL  ALA  ALA  GLY  GLU  ILE
                         ...A A G A C G T A T C C A A A A C G T T G C G G C A G G C G A A A T
                         ... 2670           2680           2690           2700

SER  ALA  THR  SER  THR  ASP  ALA  ILE  ASN...
T T C C G C T A C T T C C A C C G A T G C G A T T A A ...
          2710           2720            ...
```

FIG.18N

```
                                 ...  GLY  SER  GLN  LEU  TYR  ALA  VAL  ALA  LYS  GLY  VAL
                                 ...C G G C A G C C A G T T G T A T G C C G T G G C A A A G G G T
                                 ... 2730           2740           2750           2760

 THR  ASN  LEU  ALA  GLY  GLN  VAL  ASN  LYS...
A A C A A A C C T T G C T G G A C A A G T G A A T A A ...
           2770           2780           ...
                                 ...  VAL  GLY  LYS  ARG  ALA  ASP  ALA  GLY  THR  ALA  SER
                                 ...A G T G G G C A A A C G T G C A G A T G C A G G T A C A G C A A G
                                 ... 2790           2800           2810           2820

 ALA  LEU  ALA  ALA  SER  GLN  LEU  PRO  GLN...
T G C A T T A G C G G C T T C A C A G T T A C C A C A ...
           2830           2840           ...
                                 ...  ALA  SER  MET  SER  GLY  LYS  SER  MET  VAL  SER  ILE
                                 ...A G C C T C T A T G T C A G G T A A A T C A A T G G T T T C T A T
                                 ... 2850           2860           2870           2880

 ALA  GLY  SER  SER  TYR  GLN  GLY  GLN  SER...
T G C G G G A A G T A G T T A T C A A G G T C A A A G ...
           2890           2900           ...
                                 ...  GLY  LEU  ALA  ILE  GLY  VAL  SER  ARG  ILE  SER  ASP
                                 ...T G G T T T A G C T A T C G G G G T A T C A A G A A T T T C C G A
                                 ... 2910           2920           2930           2940
```

FIG.18O

```
ASN   GLY   LYS   VAL   ILE   ILE   ARG   LEU   SER...
T A A T G G C A A A G T G A T T A T T C G C T T G T C ...
              2950                  2960              ...
                                    ...   GLY   THR   THR   ASN   SER   GLN   GLY   LYS   THR   GLY   VAL
                                    ...A G G C A C A A C C A A T A G C C A A G G T A A A A C A G G C G T
                                    ... 2970              2980                2990                3000

ALA   ALA   GLY   VAL   GLY   TYR   GLN   TRP   ***
T G C A G C A G G T G T T G G T T A C C A G T G G T A ...
              3010                  3020              ...

                                    ...A T A G A A T T C
                                    ... 3030
```

FIG. 19A

NTHi strain 32 *hia*

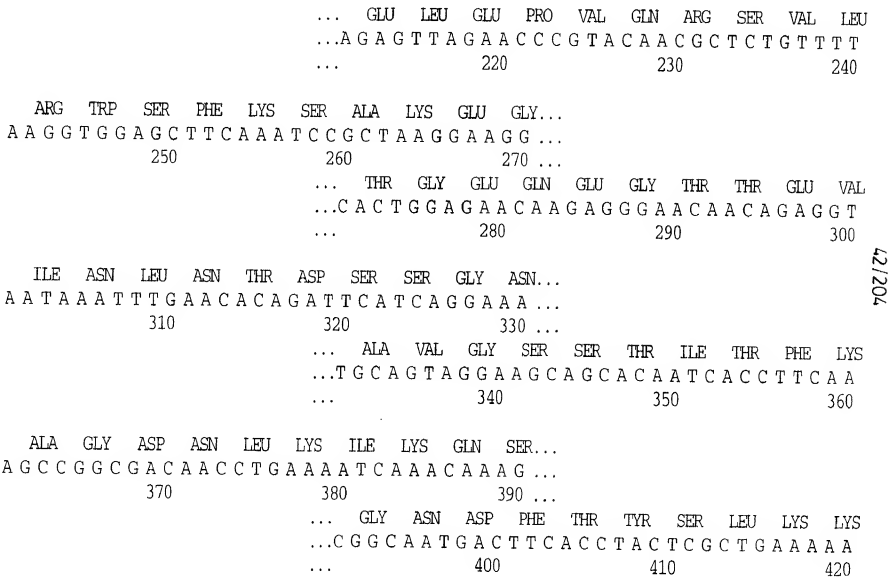
```
G A A T T C G G C T T T A A A T A T A A G G T A A A T A A A ...
                10                  20                  30 ...
                                   MET  ASN  LYS  ILE  PHE  ASN  VAL  ILE  TRP  ASN
                ...A A T G A A C A A A A A T T T T T A A C G T T A T T T G G A A
                ...                 40                  50                  60

  VAL  VAL  THR  GLN  THR  TRP  VAL  VAL  VAL  SER...
T G T T G T G A C T C A A A A C T T G G G T T G T C G T A T C  ...
                70                  80                  90 ...
                ...  GLU  LEU  THR  ARG  THR  HIS  THR  LYS  CYS  ALA
                ...T G A A C T T C A C T T C G C A C C C C A C A C C A A A T G C G C
                ...                 100                 110                 120

  SER  ALA  THR  VAL  ALA  VAL  ALA  VAL  LEU  ALA...
C T C C G C C A C C G T G G C A G T T G C C G T A T T G G C  ...
                130                 140                 150 ...
                ...  THR  LEU  LEU  SER  ALA  THR  VAL  GLN  ALA  ASN
                ...A A C C C T G T T G T C C G C A A C G G T T C A G G C G A A
                ...                 160                 170                 180

  ALA  THR  ASP  GLU  ASN  GLU  ASP  ASP  GLU  GLU...
T G C T A C C G A T G A A A A C G A A G A T G A T G A A G A  ...
                190                 200                 210 ...
```

FIG.19B


... GLU LEU GLU PRO VAL GLN ARG SER VAL LEU
...AGAGTTAGAACCCGTACAACGCTCTGTTTT
... 220 230 240
ARG TRP SER PHE LYS SER ALA LYS GLU GLY...
AAGGTGGAGCTTCAAATCCGCTAAGGAAGG ...
250 260 270 ...
... THR GLY GLU GLN GLU GLY THR THR GLU VAL
...CACTGGAGAACAAGAGGGAACAACAGAGGT
... 280 290 300
ILE ASN LEU ASN THR ASP SER SER GLY ASN...
AATAAATTTGAACACAGATTCATCAGGAAA ...
310 320 330 ...
... ALA VAL GLY SER SER THR ILE THR PHE LYS
...TGCAGTAGGAAGCAGCACAATCACCTTCAA
... 340 350 360
ALA GLY ASP ASN LEU LYS ILE LYS GLN SER...
AGCCGGCGACAACCTGAAAATCAAACAAAG ...
370 380 390 ...
... GLY ASN ASP PHE THR TYR SER LEU LYS LYS
...CGGCAATGACTTCACCTACTCGCTGAAAAA
... 400 410 420

09/936362

FIG.19C

```
   GLU  LEU  LYS  ASN  LEU  THR  SER  VAL  GLU  THR...
A G A G C T G A A A A C C T G A C C A G T G T T G A A A C ...
        430                 440                 450 ...

...  GLU  LYS  LEU  SER  PHE  GLY  ALA  ASN  GLY  ASN
...T G A A A A A T T A T C G T T T G G C G C A A A C G G C A A
...                 460                 470                 480

   LYS  VAL  ASP  ILE  THR  SER  ASP  ALA  ASN  GLY...
T A A A G T T G A T A T T A C C A G T G A T G C A A A T G G ...
        490                 500                 510 ...

...  LEU  LYS  LEU  ALA  LYS  THR  GLY  ASN  GLY  ASN
...C T T G A A A T T G G C G A A A A C A G G T A A C G G A A A
...                 520                 530                 540

   GLY  GLN  ASN  SER  ASN  VAL  HIS  LEU  ASN  GLY...
T G G T C A A A A C A G T A A T G T T C A C T T A A A C G G ...
        550                 560                 570 ...

...  ILE  ALA  SER  THR  LEU  THR  ASP  THR  LEU  ALA
...T A T T G C T T C G A C T T T G A C C G A T A C G C T T G C
...                 580                 590                 600

   GLY  GLY  THR  THR  GLY  HIS  VAL  ASP  THR  ASN...
C G G T G G C A C A A C A G G A C A C G T T G A C A C C A A ...
        610                 620                 630 ...
```

FIG.19D

```
                                ...  ILE  ASP  ALA  VAL  ASN  TYR  HIS  ARG  ALA  ALA
                                ...CATTGATGCGGTTAATTATCATCGCGCTGC
                                ...              640             650             660

  SER  VAL  GLN  ASP  VAL  LEU  ASN  SER  GLY  TRP...
AAGCGTACAAGATGTGTTAAACAGCGGTTG ...
           670             680             690 ...
                                ...  ASN  ILE  GLN  GLY  ASN  GLY  ASN  ASN  VAL  ASP
                                ...GAATATCCAAGGCAATGGAAACAATGTCGA
                                ...              700             710             720

  PHE  VAL  ARG  THR  TYR  ASP  THR  VAL  ASP  PHE...
TTTTGTCCGTACTTACGACACCGTGGACTT ...
           730             740             750 ...
                                ...  VAL  ASN  GLY  ALA  ASN  ALA  ASN  VAL  SER  VAL
                                ...TGTCAATGGCGCGAATGCCAATGTGAGCGT
                                ...              760             770             780

  THR  ALA  ASP  THR  ALA  HIS  LYS  LYS  THR  THR...
TACGGCTGATACGGCTCACAAAAAGACAAC ...
           790             800             810 ...
                                ...  VAL  ARG  VAL  ASP  VAL  THR  GLY  LEU  PRO  VAL
                                ...TGTCCGTGTGGATGTAACAGGCTTGCCGGT
                                ...              820             830             840
```

FIG.19E

```
     GLN  TYR  VAL  THR  GLU  ASP  GLY  LYS  THR  VAL...
T C A A T A T G T T A C G G A A G A C G G C A A A A C C G T ...
                850                 860                 870 ...

...  VAL  LYS  VAL  GLY  ASN  GLU  TYR  TYR  LYS  ALA
...T G T G A A A G T G G G C A A T G A G T A T T A C A A A G C
...                 880                 890                 900

     LYS  ASP  ASP  GLY  SER  ALA  ASP  MET  ASN  GLN...
C A A A G A T G A C G G T T C G G C G G A T T G A A T C A ...
                910                 920                 930 ...

...  LYS  VAL  GLU  ASN  GLY  GLU  LEU  ALA  LYS  THR
...A A A A G T C G A A A A C G G C G A G C T G G C G A A A A C
...                 940                 950                 960

     LYS  VAL  LYS  LEU  VAL  SER  ALA  SER  GLY  THR...
C A A A G T G A A A T T G G T A T C G G C A A G C G G T A C ...
                970                 980                 990 ...

...  ASN  PRO  VAL  LYS  ILE  SER  ASN  VAL  ALA  ASP
...A A A T C C G G T G A A A A A T T A G C A A T G T T G C A G A
...                1000                1010                1020

     GLY  THR  GLU  ASP  THR  ASP  ALA  VAL  SER  PHE...
C G G C A C G G A A G A C A C C G A T G C G G T C A G C T T ...
                1030                1040                1050 ...
```

FIG.19F

```
...   LYS  GLN  LEU  LYS  ALA  LEU  GLN  ASP  LYS  GLN
...T A A G C A A T T A A A A G C C T T G C A A G A C A A A C A
...             1060                1070                1080

VAL  THR  LEU  SER  THR  SER  ASN  ALA  TYR  ALA...
G G T T A C G T T G A G C A C G A G C A A T G C T T A T G C ...
          1090                1100                1110 ...

...   ASN  GLY  GLY  THR  ASP  ASN  ASP  GLY  GLY  LYS
...C A A T G G C G G T A C A G A T A A C G A C G G C G G C A A
...             1120                1130                1140

ALA  THR  GLN  THR  LEU  SER  ASN  GLY  LEU  ASN...
G G C A A C T C A A A C T T T A A G C A A T G G T T T G A A ...
          1150                1160                1170 ...

...   PHE  LYS  PHE  LYS  SER  SER  ASP  GLY  GLU  LEU
...T T T T A A A T T T A A A T C T A G C G A T G G C G A G T T
...             1180                1190                1200

LEU  LYS  ILE  SER  ALA  THR  GLY  ASP  THR  VAL...
G T T G A A A A T T A G C G C G A C C G G C G A T A C G G T ...
          1210                1220                1230 ...

...   THR  PHE  THR  PRO  LYS  LYS  GLY  SER  VAL  GLN
...T A C T T T T A C G C C G A A A A A A G G T T C G G T A C A
...             1240                1250                1260
```

FIG.19G

```
    VAL  GLY  ASP  ASP  GLY  LYS  ALA  SER  ILE  SER...
G G T T G G C G A T G A T G G C A A G G C T T C A A T T T C ...
          1270                                      1290 ...

                    ...  LYS  GLY  ALA  ASN  THR  THR  GLU  GLY  LEU  VAL
                    ...A A A A G G T G C A A A T A C A A C T G A A G G T T G G T
                    ...                                      1300                 1310                 1320

    GLU  ALA  SER  GLU  LEU  VAL  GLU  SER  LEU  ASN...
T G A G G C T T C T G A A T T G G T T G A A A G C C T G A A ...
          1330                                      1340 ...

                    ...  LYS  LEU  GLY  TRP  LYS  VAL  GLY  VAL  GLU  LYS
                    ...C A A A C T G G G T T G G A A A G T A G G G G T T G A G A A
                    ...                                      1360                 1370                 1380

    VAL  GLY  SER  GLY  GLU  LEU  ASP  GLY  THR  SER...
A G T C G G C A G C G G C G A G C T T G A T G G T A C A T C ...
          1390                                      1400 ...

                    ...  LYS  GLU  THR  LEU  VAL  LYS  SER  GLY  ASP  LYS
                    ...C A A G G A A A C T T T A G T G A A G T C G G G C G A T A A
                    ...                                      1420                 1430                 1440

    VAL  THR  LEU  LYS  ALA  GLY  ASP  ASN  LEU  LYS...
A G T A A C T T T G A A A G C C G G C G A C A A T C T G A A ...
          1450                                      1460 ...
```

FIG.19H

```
                                ... VAL LYS GLN GLU GLY THR ASN PHE THR TYR
                                ...G G T C A A A C A A G A G G G C A C A A A C T T C A C T T A
                                ...          1480          1490          1500

ALA LEU LYS ASP GLU LEU THR GLY VAL LYS...
C G C G C T C A A A G A T G A A T T G A C G G G C G T G A A ...
        1510          1520          1530 ...
                                ... SER VAL GLU PHE LYS ASP THR ALA ASN GLY
                                ...G A G C G T G G A G T T T A A A G A C A C G G C G A A T G G
                                ...          1540          1550          1560

ALA ASN GLY ALA SER THR LYS ILE THR LYS...
T G C A A A C G G T G C A A G C A C G A A G A T T A C C A A ...
        1570          1580          1590 ...
                                ... ASP GLY LEU THR ILE THR LEU ALA ASN GLY
                                ...A G A C G G C T T G A C C A T T A C G C T G G C A A A C G G
                                ...          1600          1610          1620

ALA ASN GLY ALA THR VAL THR ASP ALA ASP...
T G C G A A T G G T G C G A C G G T G A C T G A T G C C G A ...
        1630          1640          1650 ...
                                ... LYS ILE LYS VAL ALA SER ASP GLY ILE SER
                                ...C A A G A T T A A A G T T G C T T C G G A C G G C A T T A G
                                ...          1660          1670          1680
```

FIG.19I

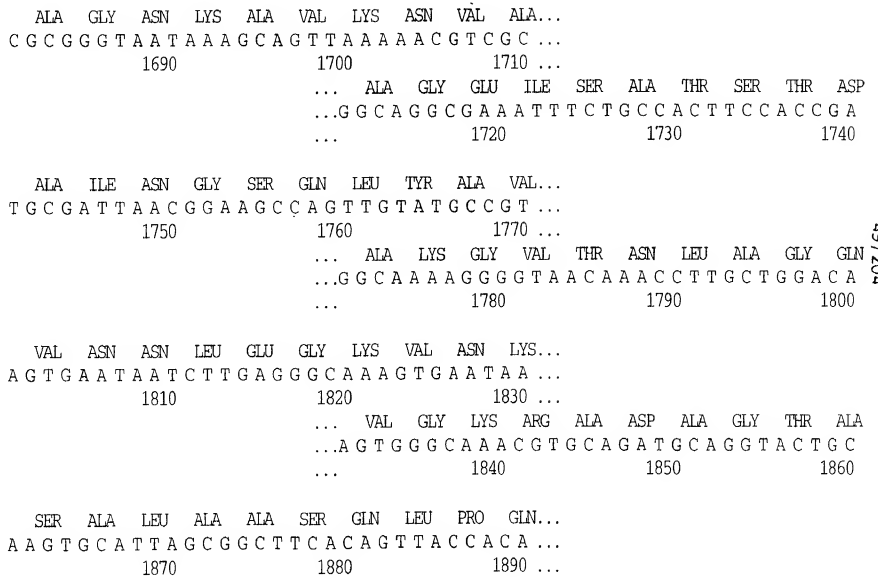


FIG.19J

```
                ...   ALA  THR  MET  PRO  GLY  LYS  SER  MET  VAL  SER
                ...A G C C A C T A T G C C A G G T A A A T C A A T G G T T T C
                ...                1900                1910                1920

      ILE  ALA  GLY  SER  SER  TYR  GLN  GLY  GLN  ASN...
T A T T G C C G G G A A G T A G T T A T C A A G G T C A A A A ...
                1930                1940                1950 ...
                ...   GLY  LEU  ALA  ILE  GLY  VAL  SER  ARG  ILE  SER
                ...T G G T T T A G C T A T C G G G G T A T C A A G A A T T T C
                ...                1960                1970                1980

      ASP  ASN  GLY  LYS  VAL  ILE  ILE  ARG  LEU  SER...
C G A T A A T G G C A A A G T G A T T A T T C G C T T G T C ...
                1990                2000                2010 ...
                ...   GLY  THR  THR  ASN  SER  GLN  GLY  LYS  THR  GLY
                ...A G G C A C A A C C A A T A G T C A A G G T A A A A C A G G
                ...                2020                2030                2040

      VAL  ALA  ALA  GLY  VAL  GLY  TYR  GLN  TRP  ***
C G T T G C C A G C C A G G T G T T G G T T A C C A G T G G T A ...

                ...A T A G A A T T C
```

FIG.20A

NTHi strain 29 Hia

```
                                    MET  ASN  LYS ...
T T A A A T A T A A G G T A A A T A A A A A T G A A C A A A...
          10                  20                  30...
                          ...  ILE  PHE  ASN  VAL  ILE  TRP  ASN  VAL  VAL  THR
                          ... A T T T T A A C G T T A T T G G A A T G T T G T G A C T
                          ...                 40                  50                  60

  GLN  THR  TRP  VAL  VAL  VAL  SER  GLU  LEU  THR ...
C A A A C T T G G G T T G T C G T A T C T G A A C T C A C T...
          70                  80                  90...
                          ...  ARG  ALA  HIS  THR  LYS  CYS  ALA  SER  ALA  THR
                          ... C G C G C C C A C A C C A A A T G C G C C T C C G C C A C C
                          ...                 100                 110                 120

  VAL  ALA  VAL  ALA  VAL  LEU  ALA  THR  ALA  LEU ...
G T G G C G G T T G C C G T A T T G G C A A C T G C C G T T G...
          130                 140                 150...
                          ...  SER  ALA  THR  ALA  GLU  ALA  ASN  ASN  ASN  THR
                          ... T C T G C A A C G G C T G A A G C G A A C A A C A A T A C T
                          ...                 160                 170                 180

  SER  VAL  THR  ASN  GLY  LEU  ASN  ALA  TYR  GLY ...
T C T G T T A C G A A T G G G T T G A A T G C T T A T G G C...
          190                 200                 210...
```

FIG.20B

```
                ... ASP THR ASN PHE ASN THR THR ASN ASN SER
                ... G A T A C T A A T T T A A T A C A A C C A A T A A A T T C G
                ...                 220                 230                 240

  ILE ALA ASP LEU GLU LYS HIS VAL GLN ASP ...
A T A G C A G A T T T G G A A A A A C A C G T T C A A G A T...
            250                 260                 270...
                ... ALA TYR LYS GLY LEU LEU ASN LEU ASN GLU
                ... G C T T A T A A A G G C T T A T T A A A T C T G A A T G A A
                ...                 280                 290                 300

LYS ASP THR ASN LYS SER SER PHE LEU VAL ...
A A A G A T A C A A A A T A A G T C A A G T T T C T T G G T T...
            310                 320                 330...
                ... ALA ASP ASN THR ALA ALA THR VAL GLY ASN
                ... G C C G A C A A A T A C C G G C C G C A A C C G T A G G C A A T
                ...                 340                 350                 360

LEU ARG LYS LEU GLY TRP VAL LEU SER SER ...
T T G C G T A A A T T G G G C T G G G T A T T G T C T A G C...
            370                 380                 390...
                ... LYS ASN GLY THR ARG ASN GLU LYS SER TYR
                ... A A A A A C G G C A C A A G G A A C G A G A A A A G C T A T
                ...                 400                 410                 420
```

FIG.20C

```
 GLN  VAL  LYS  GLN  ALA  ASP  GLU  VAL  LEU  PHE ...
CAAGTAAAACAAGCTGATGAAGTTCTCTTT...
          430                 440                 450...
                         ...  THR  GLY  SER  GLY  ALA  ALA  THR  VAL  SER  SER
                         ... ACTGGATCTGGTGCTGCAACGGTTAGTTCC
                         ...                 460                 470                 480

 SER  SER  LYS  ASP  GLY  LYS  HIS  THR  ILE  THR ...
AGCTCTAAAGACGGTAAACACATACCATTACC...
          490                 500                 510...
                         ...  ILE  SER  VAL  THR  LYS  GLY  SER  PHE  ALA  GLU
                         ... ATTCTGTTACCAAAGGTAGTTTGCTGAG
                         ...                 520                 530                 540

 VAL  LYS  THR  ASP  ALA  THR  THR  GLY  GLY  GLN ...
GTAAAAACTGATGCAACTACTGGAGGTCAA...
          550                 560                 570...
                         ...  VAL  ASN  ALA  ASP  ARG  GLY  LYS  VAL  LYS  ALA
                         ... GTAAACGCCGACCGTGGTAAAGTGAAAGCT
                         ...                 580                 590                 600

 GLU  ASP  GLU  ASN  GLY  ALA  ASP  VAL  ASP  LYS ...
GAGGACGAGAATGGAGCTGATGTTGATAAG...
          610                 620                 630...
```

FIG.20D

```
                                   ... LYS  VAL  ALA  THR  VAL  LYS  ASP  VAL  ALA  LYS
                                   ... A A A G T T G C A A C T G T A A A A G A T G T T G C T A A G
                                   ...               640                 650                 660

ALA  ILE  ASN  ASP  ALA  ALA  THR  PHE  VAL  LYS ...
G C G A T T A A C G A T G C C G C A A C T T T C G T G A A A...
               670                 680                 690...
                                   ... VAL  GLU  SER  THR  ASP  ASP  ASP  ILE  GLU  ASN
                                   ... G T G G A A A G C A C A G A T G A T G A C A T T G A A A A T
                                   ...               700                 710                 720

GLY  ALA  ALA  GLY  LYS  ASN  GLU  THR  THR  ASP ...
G G T G C T G C A G G C A A A A A T G A A A C T A C A G A C...
               730                 740                 750...
                                   ... GLN  ALA  LEU  LYS  ALA  GLY  ASP  THR  LEU  THR
                                   ... C A A G C T C T C A A A G C A G G C G A C A C C T T A A C C
                                   ...               760                 770                 780

LEU  LYS  ALA  GLY  LYS  ASN  LEU  LYS  ALA  LYS ...
T T A A A A G C G G G T A A A A A C T T A A A A G C T A A G...
               790                 800                 810...
                                   ... LEU  ASP  GLN  ASN  GLY  LYS  SER  VAL  THR  PHE
                                   ... T T A G A C C A A A A T G G T A A A T C A G T A A C C T T T
                                   ...               820                 830                 840
```

FIG.20E

```
 ALA  LEU  ALA  LYS  ASP  LEU  ASP  VAL  THR  SER ...
GCTTTAGCGAAAGACCTTGATGTGACCCTCT...
                850       860       870...

                     ...  ALA  LYS  VAL  SER  ASP  LYS  LEU  SER  ILE  GLY
                     ... GCGAAAGTGAGTGATAAGTTGTCTATTGGT
                     ...       880       890       900

 LYS  ASP  THR  ASN  LYS  VAL  ASP  ILE  THR  SER ...
AAAGATACGAATAAAGTTGATATTACCAGT...
                910       920       930...

                     ...  ASP  ALA  ASN  GLY  LEU  LYS  LEU  ALA  LYS  THR
                     ... GATGCAAATGGCTTGAAATTGGCGAAAACA
                     ...       940       950       960

 GLY  ASN  GLY  ASN  GLY  GLN  ASN  GLY  ASN  VAL ...
GGTAACGGAAATGGTCAAAACGGTAATGTC...
                970       980       990...

                     ...  HIS  LEU  ASN  GLY  ILE  ALA  SER  THR  LEU  THR
                     ... CACTTAAATGGTATTGCTTCGACTTGACC
                     ...       1000      1010      1020

 ASP  THR  ILE  THR  GLY  MET  THR  THR  GLN  ALA ...
GATACCATTACAGGTATGACAACCAAGCA...
                1030      1040      1050...
```

FIG.20F

```
                ...  SER  ASN  GLY  VAL  ALA  VAL  GLN  ASN  HIS  ASN
                ... A G C A A T G G C G T G G C T G T G C A G A A T C A T A A T
                ...                  1060                 1070                 1080

 ARG  ALA  ALA  SER  VAL  ALA  ASP  VAL  LEU  ASN ...
C G T G C T G C G A G T G T G G C T G A T G T T A A A T...
                1090                 1100                 1110...
                ...  ALA  GLY  TRP  ASN  ILE  GLN  GLY  ASN  GLY  ALA
                ... G C A G G C T G G A A T A T T C A A G G C A A C G G A G C G
                ...                  1120                 1130                 1140

 SER  VAL  ASP  PHE  VAL  ASN  ALA  TYR  ASP  THR ...
A G C G T T G A T T T T G T C A A T G C T T A C G A C A C A...
                1150                 1160                 1170...
                ...  VAL  ASP  PHE  VAL  ASN  GLY  THR  ASN  THR  ASN
                ... G T A G A T T T T G T C A A T G G T A C A A A C A C C A A T
                ...                  1180                 1190                 1200

 VAL  ASN  VAL  THR  THR  ASP  THR  ALA  HIS  LYS ...
G T G A A C G T T A C G A C T G A T A C G G C T C A C A A A...
                1210                 1220                 1230...
                ...  LYS  THR  THR  VAL  ARG  VAL  ASP  VAL  THR  GLY
                ... A A G A C A A C C G T C C G T G T G G A T G T A C A G G C
                ...                  1240                 1250                 1260
```

FIG.20G

```
 LEU  PRO  VAL  GLN  TYR  VAL  THR  GLU  ASP  GLY ...
TTGCCGGTTCAATATGTTACGGAAGACGGC...
            1270              1280              1290...
                                ... LYS  THR  VAL  VAL  LYS  VAL  ASP  ASN  LYS  TYR
                                ... AAAACCGTTGTGAAAGTGGACAATAAGTAT
                                ...           1300              1310              1320

 TYR  GLU  ALA  LYS  GLN  ASP  GLY  SER  ALA  ASP ...
TACGAAGCTAAGCAAGACGGTTCGGCGGAT...
            1330              1340              1350...
                                ... MET  ASP  LYS  LYS  VAL  GLU  ASN  GLY  GLU  LEU
                                ... ATGGATAAAAAAGTCGAAAATGGCGAGCTG
                                ...           1360              1370              1380

 ALA  LYS  THR  LYS  VAL  LYS  LEU  VAL  SER  ALA ...
GCGAAAACCAAAGTGAAATTGGTGTCGGCA...
            1390              1400              1410...
                                ... SER  GLY  GLN  ASN  PRO  VAL  LYS  ILE  SER  ASN
                                ... AGCGGTCAAAATCCGGTGAAAATCAGCAAT
                                ...           1420              1430              1440

 VAL  ALA  GLU  GLY  THR  GLU  GLU  ASN  ASP  ALA ...
GTTGCGGAAGGCACGGAAGAAAACGATGCG...
            1450              1460              1470...
```

FIG.20H

```
                                          ... VAL SER PHE LYS GLN LEU LYS ALA LEU GLN
                                          ...GTCAGCTTTAAGCAATTGAAAGCCTTGCAA
                                          ...          1480      1490      1500
GLU LYS GLN VAL THR LEU THR ALA SER ASN ...
GAGAAACAGGTTACTTTAACTGCGAGCAAT...
      1510      1520      1530...
                                          ... ALA TYR ALA ASN GLY GLY ASN ASP ALA ASP
                                          ...GCTTATGCCAATGGTGGTAACGATGCCGAC
                                          ...          1540      1550      1560
GLY GLY LYS ALA THR GLN THR LEU ASN ASN ...
GGCGGCAAGGCAACTCAAACTTTAAACAAT...
      1570      1580      1590...
                                          ... GLY LEU ASN PHE LYS PHE LYS SER THR ASP
                                          ...GGTTTGAATTTTAAATTTAAATCCACAGAC
                                          ...          1600      1610      1620
GLY GLU LEU LEU ASN ILE LYS VAL GLU ASN ...
GGCGAGTTGTTGAACATCAAAGTAGAAAAT...
      1630      1640      1650...
                                          ... ASP THR VAL THR PHE THR PRO LYS LYS GLY
                                          ...GACACAGTTACCTTTACGCCGAAAAAAGGT
                                          ...          1660      1670      1680
```

FIG.20I

```
  SER  VAL  GLN  VAL  GLY  GLU  ASP  GLY  LYS  ALA ...
T C G G T A C A G G T T G G C G A A G A C G G T A A G G C T...
                1690                      1710...
                ...  THR  ILE  GLN  ASN  GLY  THR  LYS  THR  THR  ASP
                ... A C G A T T C A A A A T G G T A C G A A A A C A A C C G A C
                ...                       1720                      1730

  GLY  LEU  VAL  GLU  ALA  SER  GLU  LEU  VAL  GLU ...
G G T T T G G T T G A A G C T T C C G A A T T G G T T G A A...
                1750                      1770...
                ... SER  LEU  ASN  LYS  LEU  GLY  TRP  LYS  VAL  GLY
                ... A G C C T T G A A C A A A C T G G G C T G G A A A G T G G G C
                ...                       1780                      1790

  VAL  ASP  LYS  ASP  GLY  SER  GLY  GLU  LEU  ASP ...
G T T G A T T A A A G A C G G C A G C G G C G A G C T T G A T...
                1810                      1820                      1830...
                ...  GLY  ALA  SER  ASN  GLU  THR  LEU  VAL  LYS  SER
                ... G G T G C A T C C A A T G A A A C T T T A G T G A A A G T C G
                ...                       1840                      1850

  GLY  ASP  LYS  VAL  THR  LEU  LYS  ALA  GLY  GLU ...
G G C G A T A A A G T A A C T T T G A A A G C C G G C G A G...
                1870                      1880                      1890...
```

FIG.20J

```
... ASN LEU LYS VAL LYS GLN ASP GLY THR ASN
... A A T C T G A A G G T C A A A C A A G A C G G C A C A A A C
...                1900                1910                1920

PHE THR TYR ALA LEU LYS ASP GLU LEU THR ...
T T C A C T T A C G C G C T C A A A G A T G A A T T G A C G...
                1930                1940                1950...
... GLY VAL LYS SER VAL GLU PHE LYS ASP THR
... G G C G T G A A G A G C G T G G A G T T T A A A G A C A C G
...                1960                1970                1980

ALA ASN GLY SER ASN GLY ALA SER THR LYS ...
G C G A A T G G T T C A A A C G G T G C A A G C A C G A A G...
                1990                2000                2010...
... ILE THR LYS ASP GLY LEU THR ILE THR SER
... A T A C C A A A G A C G G C T T G A C C A T T A C G T C G
...                2020                2030                2040

ALA ASN GLY ALA ASN GLY ALA ALA THR ...
G C A A A C G G T G C G A A T G G T G C G G C G A C T...
                2050                2060                2070...
... ASP ALA ASP LYS ILE LYS VAL ALA SER ASP
... G A T G C G G A C A A G A T T A A A G T G G C T T C A G A C
...                2080                2090                2100
```

FIG.20K

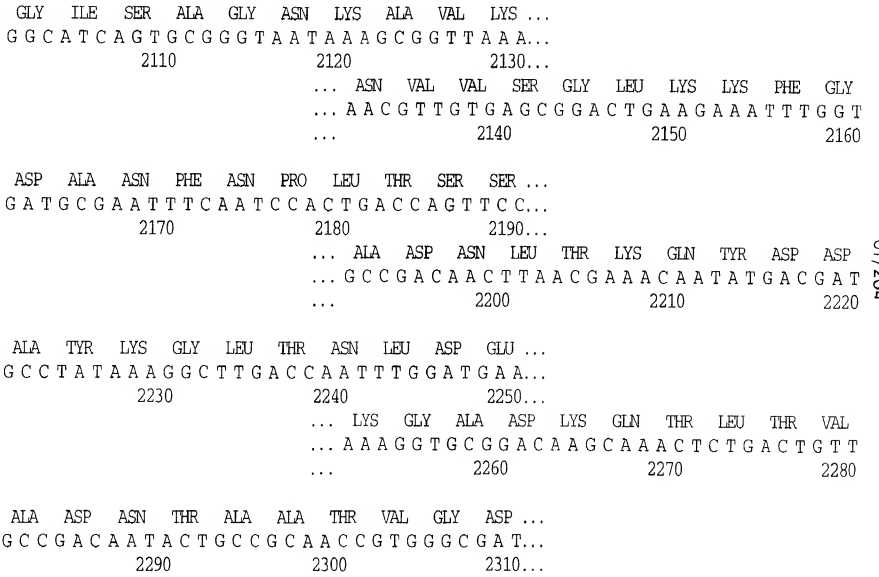


FIG.20L

```
                                ... LEU  ARG  GLY  LEU  GLY  TRP  VAL  ILE  SER  ALA
                                ... TTGCGCGGCTTGGGCTGGGTCATTTCTGCG
                                ...          2320         2330         2340

 ASP  LYS  THR  THR  GLY  GLU  LEU  ASN  LYS  GLU ...
GACAAAACCACAGGCGAACTCAATAAGGAA...
          2350         2360         2370...
                                ... TYR  ASN  ALA  GLN  VAL  ARG  ASN  ALA  ASN  GLU
                                ... TACAACGCGCAAGTGCGTAACGCCAATGAA
                                ...          2380         2390         2400

 VAL  LYS  PHE  LYS  SER  GLY  ASN  GLY  ILE  HIS ...
GTGAAATTCAAGAGCGGCAACGGTATCCAT...
          2410         2420         2430...
                                ... VAL  SER  GLY  LYS  THR  VAL  ASN  GLY  ARG  ARG
                                ... GTTTCCGGTAAAACGGTCAACGGTAGGCGC
                                ...          2440         2450         2460

 GLU  ILE  THR  PHE  GLU  LEU  ALA  LYS  ASP  GLU ...
GAAATTACTTTTGAATTGGCTAAAGACGAA...
          2470         2480         2490...
                                ... ASN  ALA  ILE  ALA  PHE  GLY  TYR  GLY  SER  LYS
                                ... AATGCCATTGCTTTCGGTTATGGCTCAAAA
                                ...          2500         2510         2520
```

FIG.20M

```
ALA  LEU  ARG  ASP  ASN  THR  VAL  ALA  ILE  GLY ...
G C C T T G C G C G A T A A C A C G G T G G C A A T T G G T...
                2530                2540                2550...

...  THR  GLY  ASN  VAL  VAL  ASN  ALA  GLU  LYS  SER
... A C G G G C A A C G T T G T G A A T G C G G A A A A T C T
...                 2560                2570                2580

GLY  ALA  PHE  GLY  ASP  PRO  ASN  TYR  ILE  GLU ...
G G T G C A T T C G G C G A T C C G A A C T A C A T C G A A...
                2590                2600                2610...

...  ASP  LYS  ALA  GLY  GLY  SER  TYR  ALA  PHE  GLY
... G A T A A A G C C G G T G G C A G C T A C G C T T C G G T
...                 2620                2630                2640

ASN  ASP  ASN  ARG  ILE  THR  SER  LYS  ASN  THR ...
A A C G A T A A C C G T A T T A C T T C T A A A A A C A C T...
                2650                2660                2670...

...  PHE  VAL  LEU  GLY  ASN  GLY  VAL  ASN  ALA  LYS
... T T T G T T G G G T A A T G G A G T T A A T G C G A A A
...                 2680                2690                2700

TYR  LYS  ALA  ASN  GLY  ASP  VAL  ASP  THR  GLU ...
T A T A A A G C C A A T G G A G A T G T T G A T A C G G A A...
                2710                2720                2730...
```

FIG.20N

```
                                  ... THR VAL THR VAL LYS ASP LYS ASP GLY LYS
                                  ... A C C G T A A C C G T T A A G G A C A A A G A C G G T A A A
                                  ...           2740                2750                2760
GLU THR THR VAL THR VAL PRO LYS ALA LEU ...
G A G A C T A C C G T T A C T G T T C C T A A A G C G T T A...
          2770                2780                2790...
                                  ... GLY ALA THR VAL GLU ASN SER VAL TYR LEU
                                  ... G G G G C T A C G G T T G A A A A C T C C G T T T A T T T G
                                  ...           2800                2810                2820
GLY ASN LYS SER THR ALA THR LYS ASP LYS ...
G G T A A T A A A T C G A C T G C G A C A A A A G A T A A G...
          2830                2840                2850...
                                  ... GLY LYS ASN LEU LYS SER ASP GLY THR ALA
                                  ... G G T A A A A A C C T G A A A T C T G A T G G T A C G G C G
                                  ...           2860                2870                2880
GLY ASN THR THR THR ALA GLY THR THR GLY ...
G G T A A C A C T A C A A C T G C T G G C A C A A C G G G T...
          2890                2900                2910...
                                  ... THR VAL ASN GLY PHE ALA GLY ALA THR ALA
                                  ... A C G G T A A A C G G C T T T G C C G G T G C A A C G G C G
                                  ...           2920                2930                2940
```

FIG.20O

```
HIS  GLY  ALA  VAL  SER  VAL  GLY  ALA  SER  GLY ...
C A C G G T G C G G T T C T G T C G G C G C A A G C G G C...
                2950                2960                2970...
                ...  GLU  GLU  ARG  ARG  ILE  GLN  ASN  VAL  ALA  ALA
                ... G A A G A A A G A C G T A T C C A A A A C G T C G C G G C A
                ...                 2980                2990                3000

GLY  GLU  ILE  SER  ALA  THR  SER  THR  ASP  ALA ...
G G C G A A A T T T C C G C C A C T T C C A C C G A T G C G...
                3010                3020                3030...
                ...  ILE  ASN  GLY  SER  GLN  LEU  TYR  ALA  VAL  ALA
                ... A T T A A C G G C A G C C A G T T G T A T G C T G T G G C A
                ...                 3040                3050                3060

LYS  GLY  VAL  THR  ASN  LEU  ALA  GLY  GLN  VAL ...
A A A G G G G T A A C A A A T C T T G C T G G A C A A G T T G...
                3070                3080                3090...
                ...  ASN  LYS  VAL  GLY  LYS  ARG  ALA  ASP  ALA  GLY
                ... A A T A A A A G T G G G C A A A C G T G C A G A T G C A G G T
                ...                 3100                3110                3120

THR  ALA  SER  ALA  LEU  ALA  ALA  SER  GLN  LEU ...
A C A G C A A G T G C A T T A G C A G C T T C A C A G T T A...
                3130                3140                3150...
```

FIG.20P

```
                                    ... PRO  GLN  ALA  SER  MET  PRO  GLY  LYS  SER  MET
                                    ... C C A C A A G C C T C T A T G C C A G G T A A A T C A A T G
                                    ...              3160              3170              3180

 VAL  SER  ILE  ALA  GLY  SER  SER  TYR  GLN  GLY ...
G T T T C T A T T G C G G G A A G T A G T T A T C A A G G T...
           3190              3200              3210...
                                    ... GLN  ASN  GLY  LEU  ALA  ILE  GLY  VAL  SER  ARG
                                    ... C A A A A T G G T T T A G C T A T C G G G G T A T C A C G A
                                    ...              3220              3230              3240

 ILE  SER  ASP  ASN  GLY  LYS  VAL  ILE  ILE  ARG ...
A T T T C C G A T A A T G G C A A A G T G A T T A T T C G C...
           3250              3260              3270...
                                    ... LEU  SER  GLY  THR  THR  ASN  SER  GLN  GLY  LYS
                                    ... T T G T C A G G C A C A A C C A A T A G C C A A G G T A A A
                                    ...              3280              3290              3300

 THR  GLY  VAL  ALA  ALA  GLY  VAL  GLY  TYR  GLN ...
A C A G G C G T T G C A G C A G G T G T T G G T T A C C A G...
           3310              3320              3330...
                                    ... TRP  ***
                                    ... T G G T A A T A G A A T T C C G G A T C C G C
                                    ...              3340              3350
```


09/936,362
PCT/CA00/00289

FIG.21A

NTHi strain M4071 Hia

```
                MET  ASN  LYS  ILE  PHE  ASN  VAL...
G C G A A T T C A T A T G A A C A A A A A T T T T T A A C G T ...
          10                                  30 ...
                ...  ILE  TRP  ASN  VAL  MET  THR  GLN  THR  TRP  ALA
                ...T A T T T G G A A T G T T A T G A C T C A A A C T T G G G C
                ...                                 40                  50                  60

     VAL  VAL  SER  GLU  LEU  THR  ARG  ALA  HIS  THR...
T G T C G T A T C T G A A C T C A C T C G C G C C C A C A C ...
                70                  80                  90 ...
                ...  LYS  ARG  ALA  SER  ALA  THR  VAL  ALA  THR  ALA
                ...C A A A C G T G C C T C C G C A A C C G T G G C A A C C G C
                ...                 100                 110                 120

     VAL  LEU  ALA  THR  LEU  LEU  SER  THR  THR  VAL...
C G T A T T G G C G A C G T T G T T G T C T A C A A C A G T ...
               130                 140                 150 ...
                ...  GLN  ALA  THR  THR  THR  GLY  GLY  THR  THR  SER
                ...T C A G G C G A C A A C T A C T G G C G G T A C G A C A A G
                ...                 160                 170                 180

     THR  ASN  GLY  LEU  LYS  ALA  TYR  GLY  SER  THR...
T A C A A A C G G T T T G A A A G C T T A T G G A A G T A C ...
               190                 200                 210 ...
```

FIG.21B

```
                                    ...  ASN  ASN  PRO  ASN  PHE  ASN  ALA  ALA  GLY  ASN
                                    ...GAATAATCCGAATTTCAATGCTGCAGGTAA
                                    ...              220             230             240

  SER  ALA  THR  ASP  LEU  ALA  ARG  GLN  PHE  ASP...
CTCTGCAACTGATTTAGCTAGACAGTTTGA...
            250             260             270 ...
                                    ...  GLY  ALA  TYR  ASP  GLY  LEU  LEU  ASN  LEU  ASN
                                    ...TGGTGCTTATGACGGTTTATTAAATCTAAA
                                    ...              280             290             300

  GLU  LYS  ASP  ALA  ASN  LYS  ASN  LEU  LEU  VAL...
TGAAAAAGATGCGAATAAAAATCTGTTGGT...
            310             320             330 ...
                                    ...  THR  ASP  ASP  LYS  ALA  ALA  THR  VAL  GLY  ASN
                                    ...GACTGATGATAAGGCGGCGACCGTAGGCAA
                                    ...              340             350             360

  LEU  ARG  LYS  LEU  GLY  TRP  VAL  LEU  SER  SER...
TTTGCGTAAATTGGGTTGGGTATTGTCTAG...
            370             380             390 ...
                                    ...  LYS  ASN  GLY  THR  ARG  ASN  GLU  LYS  SER  GLN
                                    ...TAAAAACGGCACAAGGAACGAGAAAAGCCA
                                    ...              400             410             420
```

09/936,862
PCT/CA00/00289

FIG.21C

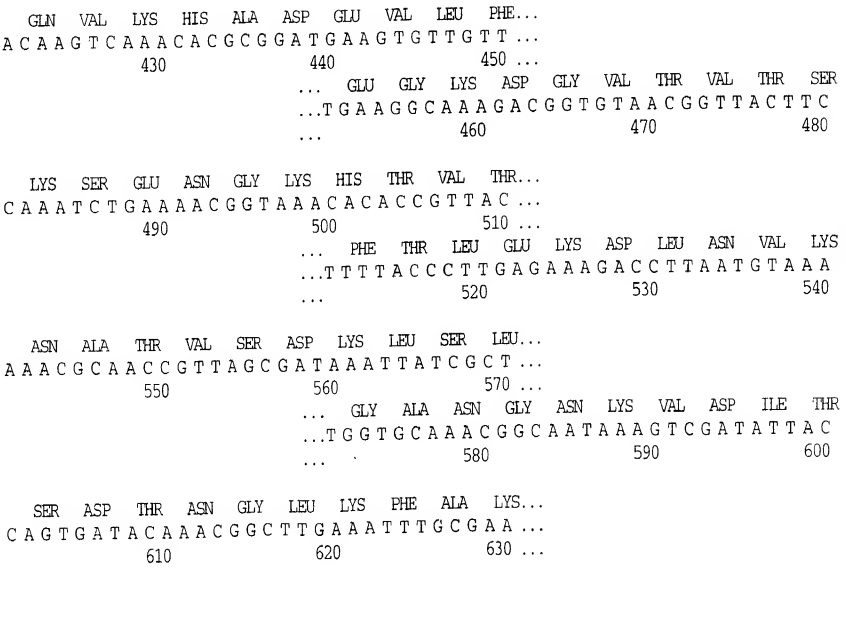

GLN VAL LYS HIS ALA ASP GLU VAL LEU PHE...
ACAAGTCAAACACGCGGATGAAGTGTTGTT...
430 440 450 ...
... GLU GLY LYS ASP GLY VAL THR VAL THR SER
...TGAAGGCAAAGACGGTGTAACGGTTACTTC
... 460 470 480
LYS SER GLU ASN GLY LYS HIS THR VAL THR...
CAAATCTGAAAACGGTAAACACACCGTTAC...
490 500 510 ...
... PHE THR LEU GLU LYS ASP LEU ASN VAL LYS
...TTTTACCCTTGAGAAAGACCTTAATGTAAA
... 520 530 540
ASN ALA THR VAL SER ASP LYS LEU SER LEU...
AAACGCAACCGTTAGCGATAAATTATCGCT...
550 560 570 ...
... GLY ALA ASN GLY ASN LYS VAL ASP ILE THR
...TGGTGCAAACGGCAATAAAGTCGATATTAC
... 580 590 600
SER ASP THR ASN GLY LEU LYS PHE ALA LYS...
CAGTGATACAAACGGCTTGAAATTTGCGAA...
610 620 630 ...

FIG.21D

```
...  PRO SER THR ASN GLY GLN ASN GLY ASN VAL
...ACCAAGTACGAATGGTCAAAACGGTAATGT
...         640        650        660

HIS LEU ASN GLY ILE ALA SER THR LEU THR...
TCACTTAAACGGTATTGCCTCTACCTTAAC...
        670        680        690...
...  ASP THR ILE THR GLY THR THR LYS SER ALA
...TGACACAATTACAGGTACAACAAAATCTGC
...         700        710        720

THR ASN GLY VAL ASP VAL GLN ASN HIS ASN...
AACTAATGGTGTAGATGTGCAGAATCATAA...
        730        740        750...
...  ARG ALA ALA SER VAL ALA ASP VAL LEU ASN
...TCGTGCTGCGAGTGTAGCTGATGTATTGAA
...         760        770        780

ALA GLY TRP ASN ILE GLN GLY ASN GLY ALA...
TGCAGGCTGGAATATTCAAGGCAACGGAGC...
        790        800        810...
...  SER VAL ASP PHE VAL ASN THR TYR ASP THR
...GAGCGTTGATTTTGTCAATACTTACGACAC
...         820        830        840
```

FIG.21E

```
   VAL  ASP  PHE  VAL  ASN  GLY  LEU  ASN  THR  ASN...
AGTAGATTTTGTCAATGGTTTAAATACCAA...
          850            860            870 ...
                    ...  VAL  ASN  VAL  THR  THR  ASP  THR  ALA  HIS  ASN
                   ...TGTGAACGTTACGACTGATACGGCTCACAA
                   ...          880            890            900

   LYS  LYS  THR  THR  VAL  ARG  VAL  ASP  VAL  THR...
CAAAAAGACAACCGTCCGTGTGGATGTAAC...
          910            920            930 ...
                    ...  GLY  LEU  PRO  VAL  GLN  TYR  VAL  THR  GLU  ASP
                   ...GGGCTTGCCGGTCCAATATGTTACGGAAGA
                   ...          940            950            960

   GLY  GLU  THR  VAL  VAL  LYS  VAL  GLY  ASN  GLU...
CGGCGAAACCGTTGTGAAAGTGGGCAATGA...
          970            980            990 ...
                    ...  TYR  TYR  GLU  ALA  LYS  GLN  ASP  GLY  SER  ALA
                   ...GTATTACGAAGCCAAGCAAGACGGTTCGGC
                   ...          1000           1010           1020

   ASP  MET  ASP  LYS  LYS  VAL  GLU  ASN  GLY  LYS...
GGATATGGATAAAAAAGTCGAAAATGGCAA...
          1030           1040           1050 ...
```


09/936,862

FIG.21F

```
                                    ...  LEU  ALA  LYS  THR  LYS  VAL  LYS  LEU  VAL  SER
                                    ...G C T G G C G A A A A C T A A A G T T A A A T T G G T A T C
                                    ...              1060              1070              1080

  ALA  ASN  GLY  THR  ASN  PRO  VAL  LYS  ILE  SER...
G G C A A A C G G T A C A A A T C C G G T G A A A A T C A G ...
          1090              1100              1110 ...
                                    ...  ASN  VAL  ALA  ASP  GLY  THR  GLU  ASN  THR  ASP
                                    ...C A A T G T T G C G G A C G G C A C G G A A A A T A C C G A
                                    ...              1120              1130              1140

  ALA  VAL  SER  PHE  LYS  GLN  LEU  LYS  ALA  LEU...
T G C G G T C A G C T T T A A G C A G T T G A A A G C C T T ...
          1150              1160              1170 ...
                                    ...  GLN  ASP  LYS  GLN  VAL  THR  LEU  SER  ALA  SER
                                    ...G C A A G A C A A A C A G G T T A C G T T A A G T G C G A G
                                    ...              1180              1190              1200

  ASN  ALA  TYR  ALA  ASN  GLY  GLY  SER  ASP  ALA...
C A A T G C T T A T G C C A A T G G C G G T A G C G A T G C ...
          1210              1220              1230 ...
                                    ...  ASP  GLY  GLY  LYS  GLY  ILE  GLN  THR  LEU  SER
                                    ...C G A C G G C G G C A A G G G A A T T C A A A C T T T A A G
                                    ...              1240              1250              1260
```

FIG.21G

```
     ASN  GLY  LEU  ASN  PHE  LYS  PHE  LYS  SER  THR...
C A A T G G T T T G A A T T T T A A A T T T A A A T C C A C ...
                1270                1280                1290 ...

                ...  ASP  GLY  GLU  LEU  LEU  ASN  ILE  LYS  ALA  GLU
                ...A G A C G G C G A G T T G T T G A A T A T C A A A G C A G A
                ...                 1300                1310                1320

     ASN  ASP  THR  VAL  THR  PHE  THR  PRO  LYS  LYS...
A A A T G A C A C G G T T A C C T T T A C G C C G A A A A A ...
                1330                1340                1350 ...

                ...  GLY  SER  VAL  GLN  VAL  GLY  ASP  ASP  GLY  LYS
                ...A G G T T C G G T G C A G G T T G G C G A T G A T G G T A A
                ...                 1360                1370                1380

     ALA  THR  ILE  GLN  ASP  GLY  ALA  LYS  THR  THR...
G G C T A C G A T T C A A G A C G G C G C A A A A A C A A C ...
                1390                1400                1410 ...

                ...  THR  GLY  LEU  VAL  GLU  ALA  SER  GLU  LEU  VAL
                ...T A C C G G T T T G G T T G A G G C T T C T G A A T T G G T
                ...                 1420                1430                1440

     ASP  SER  LEU  ASN  LYS  LEU  GLY  TRP  LYS  VAL...
T G A C A G C C T G A A C A A A T T G G G T T G G A A A G T ...
                1450                1460                1470 ...
```

FIG.21H

```
... GLY THR GLY THR ASP GLY THR GLY VAL THR
...G G G C A C C G G C A C T G A C G G C A C A G G A G T G A C
...            1480                1490                1500

ASP GLY THR HIS THR ASP THR LEU VAL LYS...
C G A T G G C A C G C A T A C C G A C A C T T T A G T G A A ...
          1510                1520                1530 ...

... SER GLY ASP LYS VAL THR LEU LYS ALA GLY
...G T C G G G C G A T A A A G T A A C T T T G A A A G C C G G
...            1540                1550                1560

ASP ASN LEU LYS VAL LYS GLN GLU GLY THR...
C G A C A A T C T G A A G G T C A A A C A A G A G G G T A C ...
          1570                1580                1590 ...

... ASN PHE THR TYR ALA LEU LYS ASP GLU LEU
...A A A C T T C A C T T A T G C G C T C A A A G A T G A A T T
...            1600                1610                1620

THR ASP VAL LYS SER VAL GLU PHE LYS ASP...
G A C G G A C G T G A A G A G C G T G G A G T T T A A A G A ...
          1630                1640                1650 ...

... THR ALA ASN GLY ALA ASN GLY ALA SER THR
...C A C G G C G A A T G G T G C A A A C G G T G C A A G C A C
...            1660                1670                1680
```

09/936362

FIG.21I

```
 LYS  ILE  THR  LYS  ASP  GLY  LEU  THR  ILE  THR...
GAAGATTACCAAAGACGGCTTGACCATTAC ...
          1690           1700           1710 ...
                         ...  PRO  ALA  ASN  GLY  ALA  GLY  ALA  ALA  GLY  ALA
                         ...GCCGGCAAACGGTGCGGGTGCGGCAGGTGC
                         ...            1720           1730           1740

 ASN  THR  ALA  ASN  THR  ILE  SER  VAL  THR  LYS...
AAACACTGCAAACACCATTAGCGTAACCAA ...
          1750           1760           1770 ...
                         ...  ASP  GLY  ILE  SER  ALA  GLY  ASN  LYS  ALA  VAL
                         ...AGACGGCATTAGCGCGGTAATAAAGCAGT
                         ...            1780           1790           1800

 LYS  ASN  VAL  VAL  SER  GLY  LEU  LYS  LYS  PHE...
TAAAAACGTTGTGAGCGGACTGAAGAAATT ...
          1810           1820           1830 ...
                         ...  GLY  ASP  ALA  ASN  PHE  ASP  PRO  LEU  THR  SER
                         ...TGGTGATGCGAATTTCGATCCGCTGACTAG
                         ...            1840           1850           1860

 SER  ALA  ASP  ASN  LEU  THR  LYS  GLN  TYR  ASP...
CTCAGCCGACAACTTAACGAAACAATATGA ...
          1870           1880           1890 ...
```

09/936362

FIG.21J

```
                              ... ASN  ALA  TYR  LYS  GLY  LEU  THR  ASN  LEU  ASP
                              ...C A A T G C C T A T A A A G G C T T G A C C A A T C T G G A
                              ...          1900            1910            1920
GLU  LYS  SER  LYS  GLY  LYS  GLN  THR  PRO  THR...
T G A A A A A A G T A A A G G C A A G C A A A C T C C G A C ...
        1930            1940            1950 ...
                              ... VAL  ALA  ASP  ASN  THR  ALA  ALA  THR  VAL  GLY
                              ...C G T T G C T G A C A A T A C C G C T G C A A C C G T G G G
                              ...          1960            1970            1980
ASP  LEU  ARG  GLY  LEU  GLY  TRP  VAL  ILE  SER...
C G A T T T G C G C G G C T T G G G C T G G G T C A T T T C ...
        1990            2000            2010 ...
                              ... ALA  ASP  LYS  THR  LYS  GLY  GLU  LEU  ASN  LYS
                              ...T G C A G A C A A A A C C A A A G G C G A A C T C A A T A A
                              ...          2020            2030            2040
GLU  TYR  ASN  ALA  GLN  VAL  ARG  ASN  ALA  ASN...
G G A A T A C A A C G C A C A A G T G C G T A A C G C T A A ...
        2050            2060            2070 ...
                              ... GLU  VAL  LYS  PHE  LYS  SER  GLY  ASN  GLY  ILE
                              ...T G A A G T G A A A T T C A A G A G C G G C A A C G G T A T
                              ...          2080            2090            2100
```

09/936362

FIG.21K

```
 ASN  VAL  SER  GLY  LYS  THR  LEU  ASP  ASN  GLY...
C A A T G T T T C C G G T A A A A C A T T G G A T A A C G G ...
             2110            2120            2130 ...
                            ...  THR  ARG  GLU  ILE  THR  PHE  GLU  LEU  ALA  LYS
                            ...T A C G C G C G A A A T T A C T T T T G A A T T G G C T A A
                            ...            2140            2150            2160

 ASP  GLU  ASN  ALA  ILE  ALA  PHE  GLY  SER  GLY...
A G A C G A A A A T G C C A T T G C T T T C G G T T C T G G ...
             2170            2180            2190 ...
                            ...  SER  LYS  ALA  LEU  ARG  ASP  ASN  THR  VAL  ALA
                            ...C T C A A A A G C C T T G C G C G A T A A C A C G G T G G C
                            ...            2200            2210            2220

 ILE  GLY  THR  GLY  ASN  VAL  VAL  ASN  ALA  GLU...
A A T T G G T A C G G G C A A C G T T G T G A A T G C G G A ...
             2230            2240            2250 ...
                            ...  LYS  SER  GLY  ALA  PHE  GLY  ASP  PRO  ASN  TYR
                            ...A A A A T C T G G T G C A T T C G G C G A T C C G A A C T A
                            ...            2260            2270            2280

 ILE  GLU  ASP  LYS  ALA  GLY  GLY  SER  TYR  ALA...
C A T C G A A G A T A A A G C C G G T G G C A G C T A C G C ...
             2290            2300            2310 ...
```

FIG.21L

```
... PHE GLY ASN ASP ASN ARG ILE THR SER LYS
...T T T C G G T A A C G A T A A C C G T A T T A C T T C T A A
...          2320                2330                2340

ASN THR PHE VAL LEU GLY ASN SER VAL ASN...
A A A C A C T T T T G T G T T G G G T A A T A G T G T T A A ...
          2350                2360                2370 ...

... ALA LYS ARG ASP ALA ASN GLY ASN VAL LEU
...T G C G A A A C G T G A T G C A A A T G G C A A T G T A C T
...          2380                2390                2400

THR GLU GLU LYS GLU VAL VAL GLY LYS ASP...
G A C C G A A G A A A A A G A A G T G G T T G G A A A A G A ...
          2410                2420                2430 ...

... GLY ALA LYS THR LYS VAL THR VAL PRO GLN
...C G G T G C G A A G A C G A A A G T A A C C G T G C C G C A
...          2440                2450                2460

ALA LEU GLY GLU THR VAL GLU ASN SER VAL...
A G C C T T A G G C G A A A C C G T A G A A A A T T C T G T ...
          2470                2480                2490 ...

... TYR LEU GLY ASN ALA SER THR ALA THR LYS
...T T A T C T C G G T A A T G C T T C A A C T G C G A C A A A
...          2500                2510                2520
```

FIG.21M

```
  ASP  LYS  GLY  LYS  ASN  LEU  LYS  SER  ASP  GLY...
A G A T A A G G G T A A A A A C C T G A A A T C T G A T G G ...
                2530                2540                2550 ...

                ...  THR  ALA  GLY  ASN  THR  THR  THR  ALA  GLY  ALA
                ...T A C G G G C G G G T A A C A C T A C A A C T G C T G G C G C
                ...                 2560                2570                2580

  THR  GLY  THR  VAL  ASN  GLY  PHE  ALA  GLY  ALA...
A A C G G G T A C G G T A A A C G G G C T T T G C C G G T G C ...
                2590                2600                2610 ...

                ...  THR  ALA  HIS  GLY  ALA  VAL  SER  VAL  GLY  ALA
                ...A A C G G G C G C A C G G T G C G G T T T C T G T C G G C G C
                ...                 2620                2630                2640

  SER  GLY  GLU  GLU  ARG  ILE  GLN  ASN  VAL...
A A G T G G C G A A G A A A G A C G T A T C C A A A A C G T ...
                2650                2660                2670 ...

                ...  ALA  ALA  GLY  GLU  ILE  SER  ALA  THR  SER  THR
                ...C G C G G C A G G C G A A A T T T C C G C T A C T T C C A C
                ...                 2680                2690                2700

  ASP  ALA  ILE  ASN  GLY  SER  GLN  LEU  TYR  ALA...
A G A T G C G A T T A A C G G T A G C C A G T T G T A T G C ...
                2710                2720                2730 ...
```

FIG.21N

```
                                    ...  VAL  ALA  LYS  GLY  VAL  THR  ASN  LEU  ALA  GLY
                                    ...T G T G G C A A A A G G G G T A A C A A A C C T T G C T G G
                                    ...                2740                2750                2760

  GLN  VAL  ASN  LYS  VAL  GLY  LYS  ARG  ALA  ASP...
A C A A G T G A A T A A A G T G G G C A A A C G T G C A G A ...
                2770                2780                2790 ...
                                    ...  ALA  GLY  THR  ALA  SER  ALA  LEU  ALA  ALA  SER
                                    ...T G C A G G G T A C A G C A A G T G C A T T A G C G G C T T C
                                    ...                2800                2810                2820

  GLN  LEU  PRO  GLN  ALA  SER  MET  PRO  GLY  LYS...
A C A G T T A C C C A C A A G C C T C T A T G C C A G G T A A ...
                2830                2840                2850 ...
                                    ...  SER  MET  VAL  SER  ILE  ALA  GLY  SER  SER  TYR
                                    ...A T C A A T G G T T T C T A T T G C G G G A A G T A G T T A
                                    ...                2860                2870                2880

  GLN  GLY  GLN  SER  GLY  LEU  ALA  ILE  GLY  VAL...
T C A A G G T C A A A G T G G T T T A G C T A T C G G G G T ...
                2890                2900                2910 ...
                                    ...  SER  ARG  ILE  SER  ASP  ASN  GLY  LYS  VAL  ILE
                                    ...A T C A A G A A T T T C C G A T A A T G G C A A A G T G A T
                                    ...                2920                2930                2940
```

FIG.21O

```
   ILE  ARG  LEU  SER  GLY  THR  THR  ASN  SER  GLN...
T A T T C G G C T T G T C A G G C A C A A C C A A T A G C C A ...
                2950                      2960 ...  2970 ...
                ...  GLY  LYS  THR  GLY  VAL  ALA  ALA  GLY  VAL  GLY
                ...A G G T A A A A A C A G G C G T T G C A G C A G G T G T T G G
                ...                    2980                2990                3000

   TYR  GLN  TRP  ***  ***  ASN  SER  GLY  SER
T T A C C A G T G G T A A T A G A A T T C C G G A T C C G C
          3010                3020                3030
```

FIG.22A

NTHi strain K9 hia sequence

```
MET  ASN  LYS  ILE  PHE  ASN  VAL  ILE  TRP  ASN ...
A T G A A C A A A A T T T T A A C G T T A T T T G G A A T...
                10                   20                  30...

...  VAL  MET  THR  GLN  THR  TRP  ALA  VAL  VAL  SER
... G T T A T G A C T C A A A C T T G G G C T G T C G T A T C T
...                  40                  50                  60

GLU  LEU  THR  ARG  ALA  HIS  THR  LYS  ARG  ALA ...
G A A C T C A C T C G C G C C C A C A C C A A A C G T G C C...
                70                   80                  90...

...  SER  ALA  THR  VAL  ALA  THR  ALA  VAL  LEU  ALA
... T C C G C A A C C G T G G C G A C C G C C G T A T T G G C G
...                 100                 110                 120

THR  GLN  LEU  SER  ALA  THR  ALA  GLU  ALA  ASN ...
A C G C A G T T G T C T G C A A C G G C T G A A G C G A A C...
                130                 140                 150...

...  SER  SER  ALA  SER  VAL  THR  SER  ARG  LEU  ASN
... A G T A G T G C T T C T G T T A C G A G T A G G T T G A A T
...                 160                 170                 180

VAL  TYR  GLY  ASP  THR  ASN  THR  LYS  PHE  ASN ...
G T T T A T G G C G A T A C G A A T A C T A A A T T C A A T...
                190                 200                 210...
```

FIG.22B

```
                                    ... ALA  ALA  ASN  ASN  SER  ILE  ALA  ASP  LEU  ASN
                                    ... GCAGCCAATAATTCAATAGCAGATTTAAAT
                                    ...              220             230             240

 LYS  GLN  ASN  ASP  GLY  VAL  HIS  ASP  GLY  LEU ...
AAACAAAATGATGGTGTTCACGATGGTTTA...
          250             260             270...
                                    ... LEU  ASN  LEU  ASN  GLU  ASN  GLY  ALA  ASN  LYS
                                    ... TTAAATCTGAATGAAAACGGTGCGAATAAA
                                    ...              280             290             300

 LYS  LEU  LEU  VAL  ASP  ASP  ASN  THR  ALA  ALA ...
AAGCTGTTGGTGGATGACAATACTGCGGCG...
          310             320             330...
                                    ... THR  VAL  GLY  ASP  LEU  ARG  LYS  LEU  GLY  TRP
                                    ... ACCGTAGGCGATTTACGTAAATTGGGCTGG
                                    ...              340             350             360

 VAL  VAL  SER  THR  LYS  ASN  GLY  LYS  GLU  ASN ...
GTCGTATCAACCAAAAATGGCAAGGAAAAT...
          370             380             390...
                                    ... GLU  LYS  SER  GLN  GLN  VAL  LYS  GLN  ALA  ASP
                                    ... GAGAAAAGCCAACAAGTCAAACAGGCGGAT
                                    ...              400             410             420
```


09/936362
PCT/CA00/00289

FIG.22C

```
 GLU  VAL  LEU  PHE  LYS  GLY  SER  LYS  GLY  GLY ...
 G A A G T G G T T G T T T A A A G G C A G C A A G G C G G T...
                430                 440                 450...
                                ... VAL  GLN  VAL  THR  SER  THR  SER  GLU  ASN  GLY
                                ... G T G C A G G T T A C T T C C A C C T C T G A A A A C G G C
                                ...                 460                 470                 480

 LYS  HIS  ALA  ILE  THR  PHE  ALA  LEU  ALA  LYS ...
 A A A C A C G C C A T T A C C T T T G C T T T A G C G A A A...
                490                 500                 510...
                                ... ASP  LEU  ASP  MET  ARG  THR  ALA  THR  VAL  SER
                                ... G A C C T T G A T A T G A G A A C T G C G A C T G T G A A G T T
                                ...                 520                 530                 540

 ASP  THR  LEU  THR  ILE  GLY  GLY  SER  THR  THR ...
 G A T A C C T T A A C G A T T G G C G G T A G T A C T A C T...
                550                 560                 570...
                                ... THR  GLY  SER  ALA  THR  THR  PRO  LYS  VAL  ASN
                                ... A C A G G T A G T G C A A C A A C C A C C A A A A G T G A A T
                                ...                 580                 590                 600

 VAL  THR  SER  THR  ALA  SER  GLY  LEU  ASN  PHE ...
 G T G A C T A G C A C G G C A A G C G G C T T G A A C T T T...
                610                 620                 630...
```

FIG.22D

```
... ALA LYS GLY ALA THR GLY ALA ASN GLY ASP
... G C G A A A G G C G C T A C A G G T G C T A A T G G C G A T
...                 640                 650                 660

THR THR VAL HIS LEU THR ASN ILE ALA SER ...
A C T A C G G T T C A C T T G A C T A A T A T T G C T T C A...
                670                 680                 690...

... THR LEU GLN ASP THR LEU LEU ASN THR GLY
... A C T T T G C A A G A T A C T C T A T T G A A T A C T G G G
...                 700                 710                 720

VAL VAL SER LYS LEU ASP GLY ASN GLY ILE ...
G T T G T G A G T A A A T T A G A T G G T A A T G G T A T T...
                730                 740                 750...

... THR ALA ASP GLU LYS LYS ARG ALA ALA SER
... A C T G C T G A C G A G A A A A A A C G T G C G G C A A G C
...                 760                 770                 780

VAL GLN ASP VAL LEU ASN SER GLY TRP ASN ...
G T T C A A G A T G T T T T A A A T A G T G G T T G G A A T...
                790                 800                 810...

... ILE LYS GLY VAL LYS THR GLY ALA THR THR
... A T C A A G G G T G T T A A A A C A G G T G C G A C G A C T
...                 820                 830                 840
```

FIG.22E

```
SER  ASP  ASN  VAL  ASP  PHE  VAL  ARG  THR  TYR ...
TCTGATAACGTTGATTTTGTCCGTACTTAC...
                850       860       870...
                ... ASP   THR  VAL  GLU  PHE  LEU  SER  GLY  SER  GLU
                ...GACACAGTTGAGTTTTTGAGCGGAAGTGAA
                ...                880       890       900

GLU  THR  THR  LEU  VAL  THR  VAL  ASP  SER  GLU ...
GAAACTTACACTGGTTACAGTGGATAGTGAA...
                910       920       930...
                ... SER  ASN  GLY  LYS  SER  THR  LYS  VAL  LYS  ILE
                ...AGTAATGGAAAATCTACTTAAAGTTAAAATC
                ...               940       950       960

GLY  ALA  LYS  THR  SER  VAL  ILE  LYS  GLU  LYS ...
GGTGCGAAGACCTCTGTTATCAAAGAAAAA...
                970       980       990...
                ... ASP   GLY  LYS  LEU  PHE  THR  GLY  LYS  ALA  ASN
                ...GACGGTAAGTTATTTACTGGAAAAGCTAAT
                ...               1000      1010      1020

LYS  ASP  THR  ASN  GLN  VAL  ALA  SER  ASN  ASN ...
AAAGACACAATCAAGTCGCAAGTAATAAT...
                1030      1040      1050...
```

FIG.22F

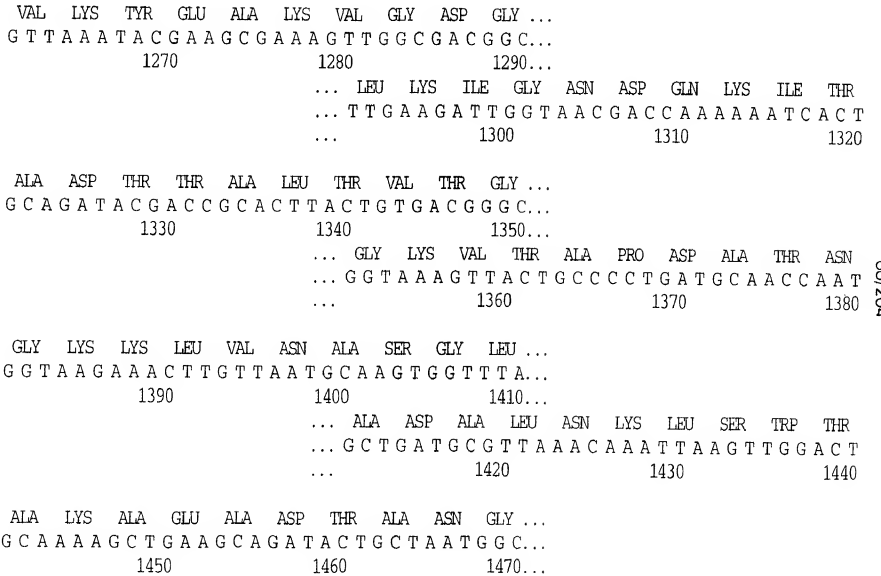
```
                                  ... ALA  ALA  ASP  ASP  THR  ASP  GLU  GLY  LYS  GLY
                                  ... G C A G C T G A T G A T A C G G A T G A G G G C A A A G G C
                                  ...           1060                1070                1080

LEU  VAL  THR  ALA  GLU  THR  VAL  ILE  ASN  ALA ...
T T A G T C A C T G C A G A G A C T G T T A T C A A T G C A...
           1090                1100                1110...
                                  ... VAL  ASN  LYS  ALA  GLY  TRP  ARG  ILE  LYS  THR
                                  ... G T A A A C A A G G C T G G T T G G A G A A T T A A A A C A
                                  ...           1120                1130                1140

THR  GLY  ALA  ASN  ASN  GLN  ALA  GLY  GLN  PHE ...
A C G G G T G C T A A T A A T C A A G C T G G T C A G T T T...
           1150                1160                1170...
                                  ... GLU  THR  VAL  THR  SER  GLY  THR  ASN  VAL  THR
                                  ... G A A A C T G T C A C A T C A G G C A C A A A T G T A A C C
                                  ...           1180                1190                1200

PHE  ALA  ASP  GLY  ASN  GLY  THR  THR  ALA  VAL ...
T T T G C T G A T G G C A A T G G T A C A A C T G C A G T C...
           1210                1220                1230...
                                  ... VAL  THR  GLY  ASP  ALA  THR  ASN  GLY  ILE  THR
                                  ... G T A A C T G G C G A T G C T A C C A A T G G T A T T A C T
                                  ...           1240                1250                1260
```

FIG.22G



09/936,062

FIG.22H

```
                              ... GLY  GLU  LEU  ASP  GLY  THR  ALA  ASP  GLU  LYS
                              ... G G C G A G C T T G A T G G A A C T G C A G A T G A A A A A
                              ...            1480                1490                1500
GLU  VAL  LYS  ALA  GLY  GLU  THR  VAL  THR  PHE ...
G A A G T T A A A G C A G G C G A A A C G G T A A C C T T T...
          1510                1520                1530...
                              ... LYS  ALA  GLY  LYS  ASN  LEU  LYS  VAL  LYS  GLN
                              ... A A A G C G G G C A A G A A C T T A A A A G T G A A A C A A
                              ...            1540                1550                1560
ASP  GLY  ALA  ASN  PHE  THR  TYR  SER  LEU  GLN ...
G A T G G T G C G A A C T T T A C T T A T T C A C T G C A A...
          1570                1580                1590...
                              ... ASP  ALA  LEU  THR  GLY  LEU  THR  SER  ILE  THR
                              ... G A T G C T T T A A C A G G C T T A A C G A G C A T T A C T
                              ...            1600                1610                1620
LEU  GLY  THR  GLY  ASN  ASN  GLY  ALA  LYS  THR ...
T T A G G T A C A G G A A A T A A T G G T G C G A A A A C T...
          1630                1640                1650...
                              ... GLU  ILE  ASN  LYS  ASP  GLY  LEU  THR  ILE  THR
                              ... G A A A T C A A C A A A G A C G G C T T A A C C A T C A C A
                              ...            1660                1670                1680
```

FIG.22I

```
  PRO  ALA  ASN  GLY  ALA  GLY  ALA  ASN  ASN  ALA ...
C C A G C A A A T G G T G C G G G T G C A A A T T A A T G C A...
                1690                1700                1710...

                ...  ASN  THR  ILE  SER  VAL  THR  LYS  ASP  GLY  ILE
                ... A A C A C C A T C A G C G T A A C C A A A G A C G G C A T T
                ...                 1720                1730                1740

  SER  ALA  GLY  GLY  GLN  SER  VAL  LYS  ASN  VAL ...
A G T G C G G G G C G G T C A G T C G G T T A A A A A C G T T...
                1750                1760                1770...

                ...  VAL  SER  GLY  LEU  LYS  LYS  PHE  GLY  ASP  ALA
                ... G T G A G C G G A C T G A A G A A A T T T G G T G A T G C G
                ...                 1780                1790                1800

  ASN  PHE  ASP  PRO  LEU  THR  SER  SER  ALA  ASP ...
A A T T T C G A T C C G C T G A C T A G C T C C G C C G A C...
                1810                1820                1830...

                ...  ASN  LEU  THR  LYS  GLN  TYR  ASP  ASP  ALA  TYR
                ... A A C T T A A C G A A A C A A T A T G A C G A T G C C T A T
                ...                 1840                1850                1860

  LYS  GLY  LEU  THR  ASN  LEU  ASP  GLU  LYS  GLY ...
A A A G G C T T G A C C A A T T T G G A T G A A A A A G G T...
                1870                1880                1890...
```

FIG.22J

```
                    ... ALA ASP LYS GLN THR LEU THR VAL ALA ASP
                    ... G C G G A C A A G C A A A C T C T G A C T G T T G C C G A C
                    ...           1900                1910                1920
ASN THR ALA ALA THR VAL GLY ASP LEU ARG ...
A A T A C T G C C G C A A C C G T G G G C G A T T T G C G C...
          1930                1940                1950...
                    ... GLY LEU GLY TRP VAL ILE SER ALA ASP LYS
                    ... G G C T T G G G C T G G G T C A T T T C T G C G G A C A A A
                    ...           1960                1970                1980
THR THR GLY GLU LEU ASP LYS GLU TYR ASN ...
A C C A C A G G C G A A C T C G A T A A G G A A T A C A A C...
          1990                2000                2010...
                    ... ALA GLN VAL ARG ASN ALA ASN GLU VAL LYS
                    ... G C G C A A G T G C G T A A C G C C A A T G A A G T G A A A
                    ...           2020                2030                2040
PHE LYS SER GLY ASN GLY ILE ASN VAL SER ...
T T C A A A A G C G G C A A C G G T A T C A A T G T T T C C...
          2050                2060                2070...
                    ... GLY LYS THR VAL ASN GLY ARG ARG GLU ILE
                    ... G G T A A A A C T G T C A A C G G T A G G C G T G A A A T T
                    ...           2080                2090                2100
```

FIG.22K

```
  THR  PHE  GLU  LEU  ALA  LYS  GLY  GLU  VAL  VAL ...
A C T T T T G A A T T G G C T A A A G G C G A A G T G G T T...
                2110                2120           2130...
                     ...  LYS  SER  ASN  GLU  PHE  THR  VAL  LYS  GLU  THR
                     ... A A A T C G A A A T G A A T T T A C T G T C A A A G A A A C C
                     ...                2140           2150                2160

  ASN  GLY  LYS  GLU  THR  SER  LEU  VAL  LYS  VAL ...
A A T G G C A A G G A A A C G A G C C T G G T T A A A G T T...
                2170                2180           2190...
                     ...  GLY  ASP  LYS  TYR  TYR  SER  LYS  GLU  ASP  ILE
                     ... G G C G A T A A A T A T T A C A G C A A A G A G G A T A T T
                     ...                2200           2210                2220

  ASP  PRO  ALA  THR  GLY  LYS  PRO  LYS  VAL  THR ...
G A C C C C A G C A A C C G G T A A A C C G A A A G T T A C A...
                2230                2240           2250...
                     ...  ASN  GLY  ASN  ALA  VAL  ALA  ALA  LYS  TYR  GLN
                     ... A A T G G C A A T G C A G T T G C T G C G A A A T A T C A A
                     ...                2260           2270                2280

  ASP  LYS  ASP  GLY  LYS  VAL  VAL  SER  ALA  ASP ...
G A T A A A G A T G G C A A A G T C G T T C T G C T G A C...
                2290                2300           2310...
```

FIG.22L

```
                                    ... GLY  SER  SER  ASN  THR  ALA  VAL  THR  LEU  THR
                                    ... GGCAGCAGCAATACCGCTGTTACCCTAACC
                                    ...              2320           2330           2340

 ASN  LYS  GLY  TYR  GLY  TYR  VAL  THR  GLY  ASN ...
AACAAAGGTTATGGCTATGTAACAGGTAAC...
           2350           2360           2370...
                                    ... GLN  VAL  ALA  ASP  ALA  ILE  ALA  LYS  SER  GLY
                                    ... CAAGTGGCAGATGCGATTGCGAAATCAGGC
                                    ...              2380           2390           2400

 PHE  GLU  LEU  GLY  LEU  ALA  ASP  ALA  GLU  LYS ...
TTTGAGCTTGGTTTGGCTGATGCAGAAAAA...
           2410           2420           2430...
                                    ... ALA  LYS  ALA  ALA  PHE  GLY  ASP  GLU  THR  LYS
                                    ... GCGAAAGCTGCGTTTGGCGATGAAACAAAA
                                    ...              2440           2450           2460

 ALA  LEU  SER  SER  ASP  LYS  LEU  GLU  THR  VAL ...
GCCTTGTCTTCTGATAAATTGGAAACCGTA...
           2470           2480           2490...
                                    ... ASN  ALA  ASN  ASP  LYS  VAL  ARG  PHE  ALA  ASN
                                    ... AATGCCAACGACAAAGTCCGTTTTGCTAAT
                                    ...              2500           2510           2520
```

FIG.22M

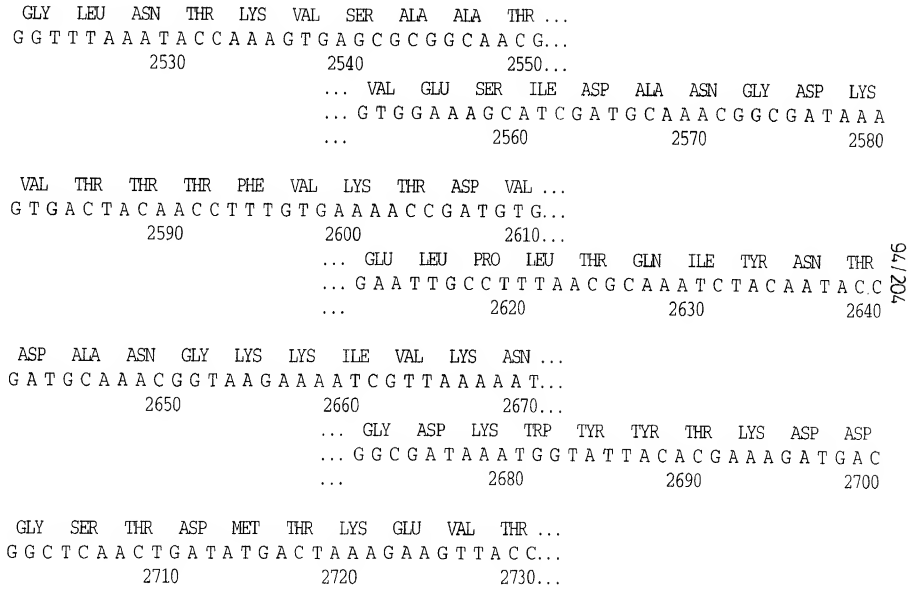


FIG.22N

```
... LEU  GLY  ASN  VAL  ASP  SER  ASP  GLY  LYS  LYS
...C T T G G C A A T G T G G A T T C A G A C G G C A A G A A A
...                2740                2750                2760

VAL  VAL  LYS  GLU  ASP  ASN  LYS  TRP  TYR  HIS ...
G T T G T G A A A G A G A C A A C A A G T G G T A T C A C...
                2770                2780                2790...
... VAL  LYS  SER  ASP  GLY  SER  THR  ASP  LYS  THR
...G T T A A A T C T G A T G G T T C T A C G G A T A A A A C A
...                2800                2810                2820

GLN  VAL  VAL  GLU  GLU  ALA  LYS  VAL  SER  THR ...
C A G G T G G T C G A A G A A G C T A A A G T T T C T A C C...
                2830                2840                2850...
... ASP  GLU  LYS  HIS  VAL  VAL  SER  LEU  ASP  PRO
...G A T G A A A A A C A C G T T G T C A G C C T T G A T C C A
...                2860                2870                2880

ASN  ASP  GLN  SER  LYS  GLY  LYS  GLY  VAL  VAL ...
A A T G A T C A A T C A A A G G T A A G G C G T G G T C...
                2890                2900                2910...
... ILE  ASN  ASN  MET  ALA  ASN  GLY  GLU  ILE  SER
...A T T A A C A A T A T G G C T A A T G G C G A A A T T C T
...                2920                2930                2940
```

FIG.22O

```
ALA  THR  SER  THR  ASP  ALA  ILE  ASN  GLY  SER ...
G C C A C T T C C A C C G A T G C G A T T A A C G G A A G T...
                2950                2960...

... GLN  LEU  TYR  ALA  VAL  ALA  LYS  GLY  VAL  THR
... C A G T T G T A T G C C G T G G C A A A G G G G T A A C A
...                 2980                2990                3000

ASN  LEU  ALA  GLY  GLN  VAL  ASN  ASN  LEU  GLU ...
A A C C T T G C T G G A C A A G T G A A T A A T C T T G A G...
          3010                3020                3030...

... GLY  LYS  VAL  ASN  LYS  VAL  GLY  LYS  ARG  ALA
... G G C A A A G T G A A T A A A G T G G G C A A A C G T G C A
...                 3040                3050                3060

ASP  ALA  GLY  THR  ALA  SER  ALA  LEU  ALA  ALA ...
G A T G C A G G T A C T G C A A G T G C A T T A G C G G C T...
          3070                3080                3090...

... SER  GLN  LEU  PRO  GLN  ALA  THR  MET  PRO  GLY
... T C A C A G T T A C C A C A A G C C A C T A T G C C A G G T
...                 3100                3110                3120

LYS  SER  MET  VAL  SER  ILE  ALA  GLY  SER  SER ...
A A A T C A A T G G T T T C T A T T G C G G G A A G T A G T...
          3130                3140                3150...
```

09/936362

FIG.22P

```
...  TYR  GLN  GLY  GLN  ASN  GLY  LEU  ALA  ILE  GLY
... T A T C A A G G T C A A A A T G G T T T A G C T A T C G G G
...                3160                3170                3180

VAL  SER  ARG  ILE  SER  ASP  ASN  GLY  LYS  VAL ...
G T A T C A A G A A T T T C C G A T A A T G G C A A A G T G...
               3190                3200                3210...
...  ILE  ILE  ARG  LEU  SER  GLY  THR  THR  ASN  SER
... A T T A T T C G C T T G T C A G G C A C A A C C A A T A G T
...                3220                3230                3240

GLN  GLY  LYS  THR  GLY  VAL  ALA  ALA  GLY  VAL ...
C A A G G T A A A A C A G G C G T T G C A G G C A G G T G T T...
               3250                3260                3270...
...  GLY  TYR  GLN  TRP  ***
... G G T T A C C A G T G G T A A T A G A A A T T C C G G A T C C
...                3280                3290                3300
```

FIG.23A

NTHi strain K22 Hia

```
                MET  ASN  LYS  ILE  PHE  ASN...
G C G A A T T C A T A T G A A C A A A A T T T T A A ...
          10                  20                  ...
                ...  VAL  ILE  TRP  ASN  VAL  VAL  THR  GLN  THR  TRP  VAL
                ...C G T T A T T T G G A A T G T T G T G A C T C A A A C T T G G G T
                ...  30                  40                  50                  60

      VAL  VAL  SER  GLU  LEU  THR  ARG  ALA  HIS...
T G T C G T A T C T G A A C T C A C T C G C G C C C A ...
          70                  80                  ...
                ...  THR  LYS  CYS  ALA  SER  ALA  THR  VAL  ALA  VAL  ALA
                ...C A C C A A A T G C G C C T C C G C C A C C G T G G C G G T T G C C
                ...  90                  100                 110                 120

      VAL  LEU  ALA  THR  ALA  LEU  SER  ALA  THR...
C G T A T T G G C A A C T G C G T T G T C T G C A A C ...
          130                 140                 ...
                ...  ALA  GLU  ALA  ASN  ASN  ASN  THR  SER  VAL  THR  ASN
                ...G G C T G A A G C G A A C A A C A A T A C T T C T G T T A C G A A
                ... 150                 160                 170                 180
```

FIG.23B

```
    GLY  LEU  ASN  ALA  TYR  GLY  ASP  THR  ASN...
T G G G T T G A A T G C T T A T G G C G A T A C T A A ...
                190                  200
                                      ...  PHE  ASN  THR  THR  ASN  ASN  SER  ILE  ALA  ASP  LEU
                                     ...T T T A A T A C A A C C A A T A A T T C G A T A G C A G A T T T
                                     ...  210                  220                  230            240

    GLU  LYS  HIS  VAL  GLN  ASP  ALA  TYR  LYS...
G G A A A A A C A C G T T C A A G A T G C T T A T A A ...
                250                  260
                                      ...  GLY  LEU  LEU  ASN  LEU  ASN  GLU  LYS  ASP  THR  ASN
                                     ...A G G C T T A T T A A A T C T G A A T G A A A A A G A T A C A A A A
                                     ...  270                  280                  290            300

    LYS  SER  SER  PHE  LEU  VAL  ALA  ASP  ASN...
T A A G T C A A G T T T C T T G G T T G C C G A C A A ...
                310                  320
                                      ...  THR  ALA  ALA  THR  VAL  GLY  ASN  LEU  ARG  LYS  LEU
                                     ...T A C C G C C C G C A A C C G T A G G C A A T T T G C G T A A A T T
                                     ...  330                  340                  350            360

    GLY  TRP  VAL  LEU  SER  SER  LYS  ASN  GLY...
G G G C T G G G T A T T G T C T A G C A A A A A C G G ...
                370                  380
```

FIG.23C

```
                                ...  THR  ARG  ASN  GLU  LYS  SER  TYR  GLN  VAL  LYS  GLN
                                ...CACAAGGAACGAGAAAAGCTATCAAGTAAAACA
                                ...  390             400             410             420

  ALA  ASP  GLU  VAL  LEU  PHE  THR  GLY  SER...
AGCTGATGAAGTTCTCTTTACTGGATC...
          430             440             ...
                                ...  GLY  ALA  ALA  THR  VAL  SER  SER  SER  SER  LYS  ASP
                                ...TGGTGCTGCAACGGTTAGTTCCAGCTCTAAAGA
                                ...  450             460             470             480

  GLY  LYS  HIS  THR  ILE  THR  ILE  SER  VAL...
CGGTAAACATACCATTACCATTTCTGT...
          490             500             ...
                                ...  THR  LYS  GLY  SER  PHE  ALA  GLU  VAL  LYS  THR  ASP
                                ...TACCAAAGGTAGTTTTGCTGAGGTAAAAACTGA
                                ...  510             520             530             540

  ALA  THR  THR  GLY  GLY  GLN  VAL  ASN  ALA...
TGCAACTACTGGAGGTCAAGTAAACGC...
          550             560             ...
                                ...  ASP  ARG  GLY  LYS  VAL  LYS  ALA  GLU  ASP  GLU  ASN
                                ...CGACCGTGGTAAAGTGAAAGCTGAGGACGAGAA
                                ...  570             580             590             600
```

FIG.23D

```
   GLY  ALA  ASP  VAL  ASP  LYS  LYS  VAL  ALA...
T GGAGCTGATGTTGATAAGAAAGTTGC ....
          610                  620
                                ...
                                ...  THR  VAL  LYS  ASP  VAL  ALA  LYS  ALA  ILE  ASN  ASP
                                ...A A C T G T A A A A G A T G T T G C T A A G G C G A T T A A C G A
                                ...  630                  640                  650            660

   ALA  ALA  THR  PHE  VAL  LYS  VAL  GLU  SER...
T GCCGCAACTTTCGTGAAAAGTGGAAAAG ...
          670                  680
                                ...
                                ...  THR  ASP  ASP  ILE  GLU  ASN  GLY  ALA  ALA  GLY
                                ...C A C A G A T G A T G A C A T T G A A A A T G G T G C T G C A G G
                                ...  690                  700                  710            720

   LYS  ASN  GLU  THR  THR  ASP  GLN  ALA  LEU...
C AAAAAATGAAACTACAGACCAAGCTCT ...
          730                  740
                                ...
                                ...  LYS  ALA  GLY  ASP  THR  LEU  THR  LEU  LYS  ALA  GLY
                                ...C A A A G C A G G C G A C A C C T T A A C C T T A A A A G C G G G
                                ...  750                  760                  770            780

   LYS  ASN  LEU  LYS  ALA  LYS  LEU  ASP  GLN...
T AAAAACTTAAAAGCTAAGTTAGACCA ...
          790                  800
                                ...
```

FIG.23E

```
... ASN GLY LYS SER VAL THR PHE ALA LEU ALA LYS
...A A A T G G T A A A T C A G T A A C C T T T G C T T T A G C G A A
... 810 820 830 840

ASP LEU ASP VAL THR SER ALA LYS VAL...
A G A C C T T G A T G T G A C C T C T G C G A A A G T ...
850 860 ...
... SER ASP LYS LEU SER ILE GLY LYS ASP THR ASN
...G A G T G A T A A G T T G T C T A T T G G T A A A G A T A C G A A
... 870 880 890 900

LYS VAL ASP ILE THR SER ASP ALA ASN...
T A A A G T T G A T A T T A C C A G T G A T G C A A A ...
910 920 ...
... GLY LEU LYS LEU ALA LYS THR GLY ASN GLY ASN
...T G G C T T G A A A T T G G C G A A A A C A G G T A A C G G A A A
... 930 940 950 960

GLY GLN ASN GLY ASN VAL HIS LEU ASN...
T G G T C A A A A C G G T A A T G T C C A C T T A A A ...
970 980 ...
... GLY ILE ALA SER THR LEU THR ASP THR ILE THR
...T G G T A T T G C T T C G A C T T T G A C C G A T A C C A T T A C
... 990 1000 1010 1020
```

FIG.23F

```
   GLY  MET  THR  THR  GLN  ALA  SER  ASN  GLY...
A G G T A T G A C A A C A C A A G C A A G T G G ...
                1030                1040
                                     ...
                                     VAL  ALA  VAL  GLN  ASN  HIS  ASN  ARG  ALA  ALA  SER
                                     ...C G T G G C T G T G C A G A A T C A T A A T C G T G C T G C G A G
                                     ... 1050                1060                1070                1080

   VAL  ALA  ASP  VAL  LEU  ASN  ALA  GLY  TRP...
T G T G G C T G A T G T A T T A A A T G C A G G C T G ...
                1090                1100
                                     ...  ASN  ILE  GLN  GLY  ASN  GLY  ALA  SER  VAL  ASP  PHE
                                     ...G A A T A T T C A A G G C A A C G G A G C G A G C G T T G A T T T
                                     ... 1110                1120                1130                1140

   VAL  ASN  ALA  TYR  ASP  THR  VAL  ASP  PHE...
T G T C A A T G C T T A C G A C A C A G T A G A T T T ...
                1150                1160
                                     ...  VAL  ASN  GLY  THR  ASN  THR  ASN  VAL  ASN  VAL  THR
                                     ...T G T C A A T G G T A C A A A C A C C A A T G T G A A C G T T A C
                                     ... 1170                1180                1190                1200

   THR  ASP  THR  ALA  HIS  LYS  LYS  THR  THR...
G A C T G A T A C G G C T C A C A A A A A G A C A A C ...
                1210                1220
                                     ...
```

FIG.23G

```
...   VAL  ARG  VAL  ASP  VAL  THR  GLY  LEU  PRO  VAL  GLN
...C G T C C G T G T G G A T G T A A C A G G C T T G C C G G T T C A
... 1230                1240                1250                1260

  TYR  VAL  THR  GLU  ASP  GLY  LYS  THR  VAL...
A T A T G T T A C G G A A G A C G G C A A A A C C G T ...
                1270                1280                ...
...   VAL  LYS  VAL  ASP  ASN  LYS  TYR  TYR  GLU  ALA  LYS
...T G T G A A A A G T G G A C A A T A A G T A T T A C G A A G C T A A
... 1290                1300                1310                1320

  GLN  ASP  GLY  SER  ALA  ASP  MET  ASP  LYS...
G C A A G A C G G T T C G G G C G G A T A T G G A T A A ...
                1330                1340                ...
...  LYS  VAL  GLU  ASN  GLY  GLU  LEU  ALA  LYS  THR  LYS
...A A A A G T C G A A A A A T G G C G A G C T G G C G A A A A C C A A
... 1350                1360                1370                1380

  VAL  LYS  LEU  VAL  SER  ALA  SER  GLY  GLN...
A G T G A A A A T T G G T C G G C A A G C G G T C A ...
                1390                1400                ...
...  ASN  PRO  VAL  LYS  ILE  SER  ASN  VAL  ALA  GLU  GLY
...A A A T C C G G T G A A A A T C A G C A A T G T T G C G G A A G G
... 1410                1420                1430                1440
```

FIG.23H

```
   THR  GLU  GLU  ASN  ASP  ALA  VAL  SER  PHE...
CACGGAAGAAACGATGCGGTCAGCTT ...
     1450                1460                ...
                        ...  LYS  GLN  LEU  LYS  ALA  LEU  GLN  GLU  LYS  GLN  VAL
                        ...TAAGCAATTGAAAGCCTTGCAAGAGAAACAGGT
                        ... 1470                1480                1490                1500

   THR  LEU  THR  ALA  SER  ASN  ALA  TYR  ALA...
TACTTTAACTGCGAGCAATGCTTATGC ...
     1510                1520                ...
                        ...  ASN  GLY  GLY  ASN  ASP  ALA  ASP  GLY  GLY  LYS  ALA
                        ...CAATGGTGGTAACGATGCCGACGGCGGCAAGGC
                        ... 1530                1540                1550                1560

   THR  GLN  THR  LEU  ASN  ASN  GLY  LEU  ASN...
AACTCAAACTTTAAACAATGGTTTGAA ...
     1570                1580                ...
                        ...  PHE  LYS  PHE  LYS  SER  THR  ASP  GLY  GLU  LEU  LEU
                        ...TTTTAAATTTAAATCCACAGACGGCGAGTTGTT
                        ... 1590                1600                1610                1620

   ASN  ILE  LYS  VAL  GLU  ASN  ASP  THR  VAL...
GAACATCAAAGTAGAAAATGACACAGT ...
     1630                1640                ...
```

09/936362

FIG.23I

```
                          ...  THR PHE THR PRO LYS LYS GLY SER VAL GLN VAL
                          ...T A C C T T T A C G C C G A A A A A A G G T T C G G T A C A G G T
                          ... 1650          1660          1670          1680

GLY GLU ASP GLY LYS ALA THR ILE GLN...
T G G C G A A G A C G G T A A G G C T A C G A T T C A ...
           1690          1700          ...
                          ...  ASN GLY THR LYS THR THR ASP GLY LEU VAL GLU
                          ...A A A T G G T A C G A A A A C A A C C G A C G G T T T G G T T G A
                          ... 1710          1720          1730          1740

ALA SER GLU LEU VAL GLU SER LEU ASN...
A G C T T C C G A A T T G G T T G A A A G C C T G A A ...
           1750          1760          ...
                          ...  LYS LEU GLY TRP LYS VAL GLY VAL ASP LYS ASP
                          ...C A A A C T G G G C T G G A A A G T G G G C G T T G A T A A A G A
                          ... 1770          1780          1790          1800

GLY SER GLY GLU LEU ASP GLY ALA SER...
C G G C A G C G G C G A G C T T G A T G G T G C A T C ...
           1810          1820          ...
                          ...  ASN GLU THR LEU VAL LYS SER GLY ASP LYS VAL
                          ...C A A T G A A A C T T T A G T G A A G T C G G G C G A T A A A G T
                          ... 1830          1840          1850          1860
```

FIG.23J

```
   THR  LEU  LYS  ALA  GLY  GLU  ASN  LEU  LYS...
A A C T T T G A A A G C C G G C G A G A A T C T G A A ...
          1870                1880                ...
                          ...  VAL  LYS  GLN  ASP  GLY  THR  ASN  PHE  THR  TYR  ALA
                          ...G G T C A A A C A A G A C G G C A C A A A C T T C A C T T A C G C
                          ... 1890                1900                1910                1920

   LEU  LYS  ASP  GLU  LEU  THR  GLY  VAL  LYS...
G C T C A A A G A T G A A T T G A C G G G C G T G A A ...
          1930                1940                ...
                          ...  SER  VAL  GLU  PHE  LYS  ASP  THR  ALA  ASN  GLY  SER
                          ...G A G C G T G G A G T T T A A A G A C A C G G C G A A T G G T T C
                          ... 1950                1960                1970                1980

   ASN  GLY  ALA  SER  THR  LYS  ILE  THR  LYS...
A A A C G G T G C A A G C A C G A A G A T T A C C A A ...
          1990                2000                ...
                          ...  ASP  GLY  LEU  THR  ILE  THR  SER  ALA  ASN  GLY  ALA
                          ...A G A C G G C T T G A C C A T T A C G T C G G C A A A C G G T G C
                          ... 2010                2020                2030                2040

   ASN  GLY  ALA  ALA  ALA  THR  ASP  ALA  ASP...
G A A T G G T G C G G C G G C G A C T G A T G C G G A ...
          2050                2060                ...
```

FIG.23K

```
...  LYS  ILE  LYS  VAL  ALA  SER  ASP  GLY  ILE  SER  ALA
...C A A G A T T A A A G T G G C T T C A G A C G G C A T C A G T G C
... 2070                2080                2090                2100

 GLY  ASN  LYS  ALA  VAL  LYS  ASN  VAL  VAL...
G G G T A A T T A A A G C G G T T A A A A A C G T T G T ...
                2110                2120                ...

...  SER  GLY  LEU  LYS  LYS  PHE  GLY  ASP  ALA  ASN  PHE
...G A G C G G G A C T G A A G A A A T T T G G T G A T G C G A A T T T
... 2130                2140                2150                2160

 ASN  PRO  LEU  THR  SER  SER  ALA  ASP  ASN...
C A A T C C A C T G A C C A G T T C C G C C G A C A A ...
                2170                2180                ...

...  LEU  THR  LYS  GLN  TYR  ASP  ASP  ALA  TYR  LYS  GLY
...C T T A A C G A A A C A A T A T G A C G A T G C C T A T A A A G G
... 2190                2200                2210                2220

 LEU  THR  ASN  LEU  ASP  GLU  LYS  GLY  ALA...
C T T G A C C A A T T T G G A T G A A A A A G G T G C ...
                2230                2240                ...

...  ASP  LYS  GLN  THR  LEU  THR  VAL  ALA  ASP  ASN  THR
...G G A C A A G C A A A C T C T G A C T G T T G C C G A C A A T A C
... 2250                2260                2270                2280
```

FIG.23L

```
 ALA  ALA  THR  VAL  GLY  ASP  LEU  ARG  GLY...
T G C C G C A A C C G T G G G C G A T T T G C G C G G ...
          2290                2300                 ...
                   ... LEU  GLY  TRP  VAL  ILE  SER  ALA  ASP  LYS  THR  THR
                   ...C T T G G G C T G G G T C A T T T C T G C G G A C A A A A C C A C
                   ... 2310            2320              2330              2340

 GLY  GLU  LEU  ASN  LYS  GLU  TYR  ASN  ALA...
A G G C G A A C T C A A T A A G G A A T A C A A C G C ...
          2350                2360                 ...
                   ... GLN  VAL  ARG  ASN  ALA  ASN  GLU  VAL  LYS  PHE  LYS
                   ...G C A A G T G C G T A A C G C C A A T G A A G T G A A A T T C A A
                   ... 2370            2380              2390              2400

 SER  GLY  ASN  GLY  ILE  HIS  VAL  SER  GLY...
G A G C G G C A A C G G T A T C C A T G T T T C C G G ...
          2410                2420                 ...
                   ... LYS  THR  VAL  ASN  GLY  ARG  ARG  GLU  ILE  THR  PHE
                   ...T A A A A C G G T C A A C G G T A G G C G C G A A A T T A C T T T
                   ... 2430            2440              2450              2460

 GLU  LEU  ALA  LYS  ASP  GLU  ASN  ALA  ILE...
T G A A T T G G C T A A A G A C G A A A A T G C C A T ...
          2470                2480                 ...
```

FIG.23M

```
                ...  ALA  PHE  GLY  TYR  GLY  SER  LYS  ALA  LEU  ARG  ASP
                ...T G C T T T C G G T T A T G G C T C A A A A G C C T T G C G C G A
                ... 2490                2500                2510                2520

  ASN  THR  VAL  ALA  ILE  GLY  THR  GLY  ASN...
T A A C A C G G T G G C A A T T G G T A C G G G C A A ...
                2530                2540                ...
                ...  VAL  VAL  ASN  ALA  GLU  LYS  SER  GLY  ALA  PHE  GLY
                ...C G T T G T G A A T G C G G A A A A A T C T G G T G C A T T C G G
                ... 2550                2560                2570                2580

  ASP  PRO  ASN  TYR  ILE  GLU  ASP  LYS  ALA...
C G A T C C G A A C T A C A T C G A A G A T A A A G C ...
                2590                2600                ...
                ...  GLY  GLY  SER  TYR  ALA  PHE  GLY  ASN  ASP  ASN  ARG
                ...C G G T G G C A G C T A C G C T T T C G G T T A A C G A T A A C C G
                ... 2610                2620                2630                2640

  ILE  THR  SER  LYS  ASN  THR  PHE  VAL  LEU...
T A T T A C T T C T T A A A A A C A C T T T G T G T T ...
                2650                2660                ...
                ...  GLY  ASN  GLY  VAL  ASN  ALA  LYS  TYR  LYS  ALA  ASN
                ...G G G T A A T G G A G T T A A T G C G A A A T A T A A A G C C A A
                ... 2670                2680                2690                2700
```

FIG.23N

```
   GLY  ASP  VAL  ASP  THR  GLU  THR  VAL  THR...
TGGAGATGTTGATACGGAAACCGTAAC...
          2710           2720          ...
                      ... VAL  LYS  ASP  LYS  ASP  GLY  LYS  GLU  THR  THR  VAL
                      ...CGTTAAGGACAAAGACGGTAAAGAGACTACCGT
                      ... 2730           2740           2750           2760

   THR  VAL  PRO  LYS  ALA  LEU  GLY  ALA  THR...
TACTGTTCCTAAAGCGTTAGGGGCTAC...
          2770           2780          ...
                      ... VAL  GLU  ASN  SER  VAL  TYR  LEU  GLY  ASN  LYS  SER
                      ...GGTTGAAAACTCCGTTTATTTGGGTAATAAATC
                      ... 2790           2800           2810           2820

   THR  ALA  THR  LYS  ASP  LYS  GLY  LYS  ASN...
GACTGCGACAAAAGATAAGGGTAAAAA...
          2830           2840          ...
                      ... LEU  LYS  SER  ASP  GLY  THR  ALA  GLY  ASN  THR  THR
                      ...CCTGAAATCTGATGGTACGGCGGGTAACACTAC
                      ... 2850           2860           2870           2880

   THR  ALA  GLY  THR  THR  GLY  THR  VAL  ASN...
AACTGCTGGCACAACGGGTACGGTAAA...
          2890           2900          ...
```

09/936362

FIG.23O

```
                ...  GLY  PHE  ALA  GLY  ALA  THR  ALA  HIS  GLY  ALA  VAL
                ...C G G C T T G C C G G T G C A A C G G C G C A C G G T G C G G T
                ... 2910                2920                2930                2940

      SER  VAL  GLY  ALA  SER  GLY  GLU  GLU  ARG...
T T C T G T C G G C G C A A G C G G C G A A G A A A G ...
                2950                2960
                                    ...
                ...  ARG  ILE  GLN  ASN  VAL  ALA  ALA  GLY  GLU  ILE  SER
                ...A C G T A T C C A A A A C G T C G C G G C A G G C G A A A T T T C
                ... 2970                2980                2990                3000

      ALA  THR  SER  THR  ASP  ALA  ILE  ASN  GLY...
C G C C A C T T C C A C C G A T G C G A T T A A C G G ...
                3010                3020
                                    ...
                ...  SER  GLN  LEU  TYR  ALA  VAL  ALA  LYS  GLY  VAL  THR
                ...C A G C C A G T T G T A T G C T G T G G C A A A G G G G T A A C
                ... 3030                3040                3050                3060

      ASN  LEU  ALA  GLY  GLN  VAL  ASN  LYS  VAL...
A A A T C T T G C T G G A C A A G T G A A T A A A G T ...
                3070                3080
                                    ...
                ...  GLY  LYS  ARG  ALA  ASP  ALA  GLY  THR  ALA  SER  ALA
                ...G G G C A A A C G T G C A G A T G C A G G T A C A G C A A G T G C
                ... 3090                3100                3110                3120
```

FIG.23P

```
   LEU  ALA  ALA  SER  GLN  LEU  PRO  GLN  ALA...
A T T A G C A G C T T C A C A G T T A C C A C A A G C ...
          3130                 ...
                               ...  SER  MET  PRO  GLY  LYS  SER  MET  VAL  SER  ILE  ALA
                               ...C T C T A T G C C A G G T A A A T C A A T G G T T C T A T T G C
                               ... 3150                 3160                 3170          3180

   GLY  SER  SER  TYR  GLN  GLY  GLN  ASN  GLY...
G G G A A G T A G T T A T C A A G G T C A A A A T G G ...
          3190                 ...
                               ...  LEU  ALA  ILE  GLY  VAL  SER  ARG  ILE  SER  ASP  ASN
                               ...T T T A G C T A T C G G G G T A T C A C G A A T T C C G A T A A
                               ... 3210                 3220                 3230          3240

   GLY  LYS  VAL  ILE  ILE  ARG  LEU  SER  GLY...
T G G C A A A G T G A T T A T T C G C T T G T C A G G ...
          3250                 ...
                               ...  THR  THR  ASN  SER  GLN  GLY  LYS  THR  GLY  VAL  ALA
                               ...C A C A A C C A A T A G C C A A G G T A A A A C A G G C G T T G C
                               ... 3270                 3280                 3290          3300

   ALA  GLY  VAL  GLY  TYR  GLN  TRP  ***
A G C A G G T G T T G G T T A C C A G T G G T A A T A ...
          3310                 3320                 ...

                               ...G A A T T G A T C C G C
                               ... 3330
```

09/936362

FIG.24A

H. influenzae type c strain API *hia* sequence

```
MET  ASN  LYS  ILE  PHE  ASN  VAL  ILE  TRP  ASN ...
ATG AAC AAA ATT TTT TAA CGT TAT TGG AAT...
                10                  20...

...  VAL  MET  THR  GLN  THR  TRP  VAL  VAL  VAL  SER
... GTT ATG ACT CAA ACT TGG GTT GTC GTA TCT
...                 40                  50                  60

GLU  LEU  THR  ARG  THR  HIS  THR  LYS  ARG  ALA ...
GAA CTC ACT CGC ACC CAC ACC AAA CGC GCC...
                70                  80...

...  SER  ALA  THR  VAL  GLU  THR  ALA  VAL  LEU  ALA
... TCC GCA ACC GTG GAG ACC GCC GTA TTG GCG
...                 100                 110                 120

THR  LEU  LEU  PHE  ALA  THR  VAL  GLN  ALA  ASN ...
ACA CTG TTG TTT GCA ACG GTT CAG GCG AAT...
                130                 140...

...  ALA  THR  ASP  GLU  ASP  GLU  GLU  LEU  ASP  PRO
... GCT ACC GAT GAA GAT GAA GAG GTT AGA CCC C
...                 160                 170                 180

VAL  VAL  ARG  THR  ALA  PRO  VAL  LEU  SER  PHE ...
GTA GTA CGC ACT GCC CCG TTG AGC TTC...
                190                 200...
```

FIG.24B

```
                                    ... HIS  SER  ASP  LYS  GLU  GLY  THR  GLY  GLU  LYS
                                    ... CATTCCGATAAAGAAGGCACGGGAGAAAAA
                                    ...              220            230            240

 GLU  VAL  THR  GLU  ASN  SER  ASN  TRP  GLY  ILE ...
GAAGTTACAGAAAATTCAAATTGGGGAATA...
          250            260            270...
                                    ... TYR  PHE  HIS  ASN  LYS  GLY  VAL  LEU  LYS  ALA
                                    ... TATTTCCACAATAAAGGAGTACTAAAAGCC
                                    ...              280            290            300

 GLY  ALA  ILE  THR  LEU  LYS  ALA  GLY  ASP  ASN ...
GGAGCAATCACCCTCAAAGCCGGCGACAAC...
          310            320            330...
                                    ... LEU  LYS  ILE  LYS  GLN  SER  THR  ASN  ALA  SER
                                    ... CTGAAAATCAAACAAAGCACCAATGCCAGT
                                    ...              340            350            360

 SER  PHE  THR  TYR  SER  LEU  LYS  LYS  ASP  LEU ...
AGCTTCACCTACTCGCTGAAAAAAGACCTC...
          370            380            390...
                                    ... THR  ASP  LEU  THR  SER  VAL  ALA  THR  GLU  LYS
                                    ... ACAGATCTGACCAGTGTTGCAACTGAAAAA
                                    ...              400            410            420
```

FIG.24C

```
 LEU  SER  PHE  GLY  ALA  ASN  GLY  ASP  LYS  VAL ...
TTATCGTTTGGCGCAAACGGCGATAAAGTT...
          430                 440                 450...

                         ...  ASP  ILE  THR  SER  ASP  ALA  ASN  GLY  LEU  LYS
                         ...  GATATTACCCAGTGATGCAAATGGCTTGAAA
                         ...                 460                 470                 480

 LEU  ALA  LYS  THR  GLY  ASN  GLY  ASN  VAL  HIS ...
TTGGCGAAAACAGGTAACGGAAATGTTCAT...
          490                 500                 510...

                         ...  LEU  ASN  GLY  LEU  ASP  SER  THR  LEU  PRO  ASP
                         ...  TTGAATGGTTGGATTCAACTTGCCTGAT
                         ...                 520                 530                 540

 ALA  VAL  THR  ASN  THR  GLY  VAL  LEU  SER  SER ...
GCGGTAACGAATACAGGTGTTAAGTTCA...
          550                 560                 570...

                         ...  SER  SER  PHE  THR  PRO  ASN  ASP  VAL  GLU  LYS
                         ...  TCAAGTTTTACACCTAATGATGTTGAAAAA
                         ...                 580                 590                 600

 THR  ARG  ALA  ALA  THR  VAL  LYS  ASP  VAL  LEU ...
ACAAGAGCTGCAACTGTTAAAGATGTTTTA...
          610                 620                 630...
```

FIG.24D

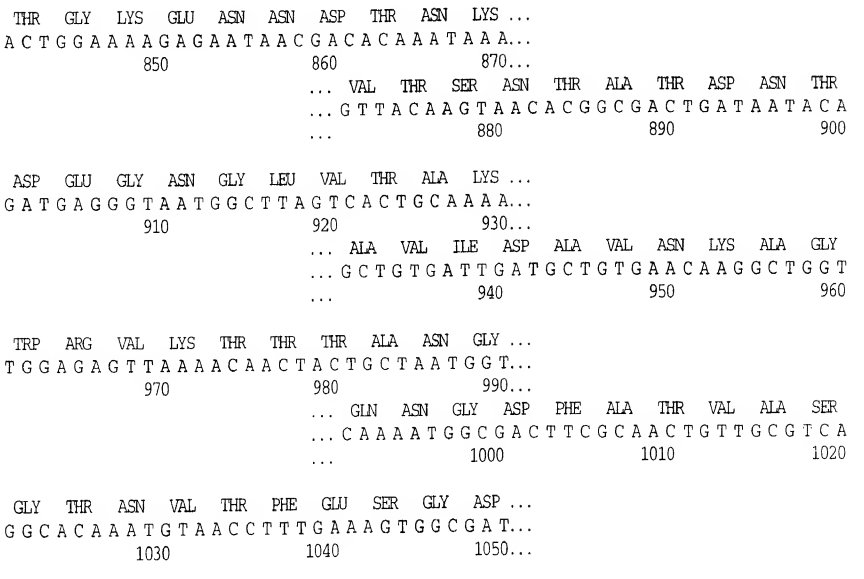
```
                                   ... ASN  ALA  GLY  TRP  ASN  ILE  LYS  GLY  ALA  LYS
                                   ... A A T G C A G G T T G G A A C A T T A A A G G T G C T A A A
                                   ...                 640                 650                 660

THR  ALA  GLY  GLY  ASN  VAL  GLU  SER  VAL  ASP ...
A C T G C T G G A G G T A A T G T T G A G A G T G T T G A T...
             670                 680                 690...
                                   ... LEU  VAL  SER  ALA  TYR  ASN  ASN  VAL  GLU  PHE
                                   ... T T A G T G T C C G C T T A T A A T A A T G T T G A A T T T
                                   ...                 700                 710                 720

ILE  THR  GLY  ASP  LYS  ASN  THR  LEU  ASP  VAL ...
A T T A C A G G C G A T A A A A A C A C G C T T G A T G T T...
             730                 740                 750...
                                   ... VAL  LEU  THR  ALA  LYS  GLU  ASN  GLY  LYS  THR
                                   ... G T A T T A A C A G C T A A A G A A A A C G G T A A A A C A
                                   ...                 760                 770                 780

THR  GLU  VAL  LYS  PHE  THR  PRO  LYS  THR  SER ...
A C C G A A G T G A A A T T C A C A C C G A A A A C C T C T...
             790                 800                 810...
                                   ... VAL  ILE  LYS  GLU  LYS  ASP  GLY  LYS  LEU  PHE
                                   ... G T T A T C A A A G A A A A A G A C G G T A A G T T A T T T
                                   ...                 820                 830                 840
```

FIG.24E



09/936362

FIG.24F

```
... GLY THR THR ALA SER VAL THR LYS ASP THR
... G G T A C A A C A G C G T C A G T A A C T A A A G A T A C T
...             1060                1070                1080

ASN GLY ASN GLY ILE THR VAL LYS TYR ASP ...
A A C G G C A A T G G C A T C A C T G T T A A G T A C G A C...
          1090                1100                1110...
... ALA LYS VAL GLY ASP GLY LEU LYS PHE ASP
... G C G A A A G T T G G C G A C G G C T T G A A A T T T G A T
...             1120                1130                1140

SER ASP LYS LYS ILE VAL ALA ASP THR THR ...
A G C G A T A A A A A A A T C G T T G C A G A T A C G A C C...
          1150                1160                1170...
... ALA LEU THR VAL THR GLY GLY LYS VAL ALA
... G C A C T T A C T G T G A C A G G T G G T A A G G T A G C T
...             1180                1190                1200

GLU ILE ALA LYS GLU ASP ASP LYS LYS LYS ...
G A A A T T G C T A A A G A A G A T G A C A A G A A A A A A...
          1210                1220                1230...
... LEU VAL ASN ALA GLY ASP LEU VAL THR ALA
... C T T G T T A A T G C A G G C G A T T T G G T A A C A G C T
...             1240                1250                1260
```

FIG.24G

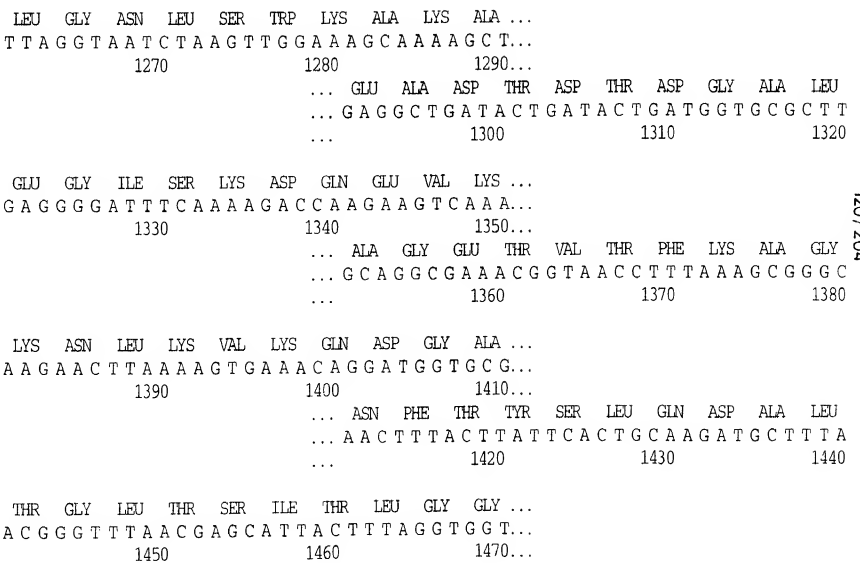


FIG.24H

```
                                ... THR  THR  ASN  GLY  GLY  ASN  ASP  ALA  LYS  THR
                                ... ACAACTAATGGCGGAAATGATGCGAAAACC
                                ...                1480           1490           1500

 VAL  ILE  ASN  LYS  ASP  GLY  LEU  THR  ILE  THR ...
GTCATCAACAAAGACGGTTTAACCATCACG...
               1510           1520           1530...
                                ... PRO  ALA  GLY  ASN  GLY  GLY  THR  THR  GLY  THR
                                ... CCAGCAGGTAATGGCGGTACGACAGGTACA
                                ...                1540           1550           1560

 ASN  THR  ILE  SER  VAL  THR  LYS  ASP  GLY  ILE ...
AACACCATCAGCGTAACCAAAGATGGCATT...
               1570           1580           1590...
                                ... LYS  ALA  GLY  ASN  LYS  ALA  ILE  THR  ASN  VAL
                                ... AAAGCAGGTAATAAAGCTATTACTAATGTT
                                ...                1600           1610           1620

 ALA  SER  GLY  LEU  ARG  ALA  TYR  ASP  ASP  ALA ...
GCGAGTGGTTTAAGAGCTTATGACGATGCG...
               1630           1640           1650...
                                ... ASN  PHE  ASP  VAL  LEU  ASN  ASN  SER  ALA  THR
                                ... AATTTTGATGTTTTAAATAACTCTGCAACT
                                ...                1660           1670           1680
```

FIG.24I

```
 ASP  LEU  ASN  ARG  HIS  VAL  GLU  ASP  ALA  TYR ...
G A T T T A A A T A G A C A C G T T G A A G A T G C T T A T...
            1690              1700              1710...
                              ... LYS  GLY  LEU  LEU  ASN  LEU  ASN  GLU  LYS  ASN
                              ... A A A G G T T T A T T A A A T C T A A A T G A A A A A A A T
                              ...              1720              1730              1740

 ALA  ASN  LYS  GLN  PRO  LEU  VAL  THR  ASP  SER ...
G C A A A T A A A C A A C C G T T G G T G A C T G A C A G C...
            1750              1760              1770...
                              ... THR  ALA  ALA  THR  VAL  GLY  ASP  LEU  ARG  LYS
                              ... A C G G C G G C G A C T G T A G G C G A T T T A C G T A A A
                              ...              1780              1790              1800

 LEU  GLY  TRP  VAL  VAL  SER  THR  LYS  ASN  GLY ...
T T G G G T T G G G T A G T A T C A A C C A A A A A C G G T...
            1810              1820              1830...
                              ... THR  LYS  GLU  GLU  SER  ASN  GLN  VAL  LYS  GLN
                              ... A C G A A A G A A G A A A G C A A T C A A G T T A A A C A A
                              ...              1840              1850              1860

 ALA  ASP  GLU  VAL  LEU  PHE  THR  GLY  ALA  GLY ...
G C T G A T G A A G T C C T C T T T A C C G G A G C C G G T...
            1870              1880              1890...
```

09/936362

FIG.24J

```
... ALA  ALA  THR  VAL  THR  SER  LYS  SER  GLU  ASN
... G C T G C T A C G G T T A C T T C C A A A T C T G A A A A C
...              1900                1910                1920

GLY  LYS  HIS  THR  ILE  THR  VAL  SER  VAL  ALA ...
G G T A A A C A T A C G A T T A C C G T T A G T G G C T...
          1930                1940                1950...
... GLU  THR  LYS  ALA  ASP  SER  GLY  LEU  GLU  LYS
... G A A A C T A A A G C G G A T A G C G G T C T T G A A A A A
...              1960                1970                1980

ASP  GLY  ASP  THR  ILE  LYS  LEU  LYS  VAL  ASP ...
G A T G G C G A T A C T A T T A A G C T C A A A G T G G A T...
          1990                2000                2010...
... ASN  GLN  ASN  THR  ASP  ASN  VAL  LEU  THR  VAL
... A A T C A A A A C A C T G A T A A T G T T T T A A C T G T T
...              2020                2030                2040

GLY  ASN  ASN  GLY  THR  ALA  VAL  THR  LYS  GLY ...
G G T A A T A A T G G T A C T G C T G T C A C T A A A G G T...
          2050                2060                2070...
... GLY  PHE  GLU  THR  VAL  LYS  THR  GLY  ALA  THR
... G G C T T T G A A A C T G T T A A A A C T G G A G C G A C T
...              2080                2090                2100
```

FIG.24K

```
 ASP  ALA  ASP  ARG  GLY  LYS  VAL  THR  VAL  LYS ...
GATGCAGATCGCGGTAAAGTAACTGTAAAA...
           2110          2120          2130...
                         ... ASP  ALA  THR  ALA  ASN  ASP  ALA  ASP  LYS  LYS
                         ...GATGCTACTGCTAATGACGCTGATAAGAAA
                         ...          2140          2150          2160

 VAL  ALA  THR  VAL  LYS  ASP  VAL  ALA  THR  ALA ...
GTCGCAACTGTAAAAGATGTTGCAACCGCA...
           2170          2180          2190...
                         ... ILE  ASN  SER  ALA  ALA  THR  PHE  VAL  LYS  THR
                         ...ATTAATAGTGCGGCGACTTTTGTGAAAACA
                         ...          2200          2210          2220

 GLU  ASN  LEU  THR  THR  SER  ILE  ASP  GLU  ASP ...
GAGAATTTAACTACCTCTATTGATGAAGAT...
           2230          2240          2250...
                         ... ASN  PRO  THR  ASP  ASN  GLY  LYS  ASP  ASP  ALA
                         ...AATCCTACAGATAACGGCAAAGATGACGCA
                         ...          2260          2270          2280

 LEU  LYS  ALA  GLY  ASP  THR  LEU  THR  PHE  LYS ...
CTTAAAGCGGGCGATACCTTAACCTTTAAA...
           2290          2300          2310...
```

09/936362

FIG.24L

```
                                ... ALA GLY LYS ASN LEU LYS VAL LYS ARG ASP
                                ... G C A G G T A A A A A C C T G A A A G T T A A A C G T G A T
                                ...             2320                2330                2340

GLY LYS ASN ILE THR PHE ASP LEU ALA LYS ...
G G A A A A A A T A T T A C T T T T G A C T T G G C G A A A...
            2350                2360                2370...
                                ... ASN LEU GLU VAL LYS THR ALA LYS VAL SER
                                ... A A C C T T G A G G T G A A A A C T G C G A A A G T G A G T
                                ...             2380                2390                2400

ASP THR LEU THR ILE GLY GLY ASN THR PRO ...
G A T A C T T T A A C G A T T G G C G G G A A T A C A C C T...
            2410                2420                2430...
                                ... THR GLY GLY THR THR ALA THR PRO LYS VAL
                                ... A C A G G T G G C A C T A C T G C G A C G C C A A A A G T G
                                ...             2440                2450                2460

ASN ILE THR SER THR ALA ASP GLY LEU ASN ...
A A T A T T A C T A G C A C G G C T G A T G G T T T G A A T...
            2470                2480                2490...
                                ... PHE ALA LYS GLU THR ALA ASP ALA SER GLY
                                ... T T T G C A A A A G A A A C A G C C G A T G C C T C G G G T
                                ...             2500                2510                2520
```

FIG.24M

```
SER  LYS  ASN  VAL  TYR  LEU  LYS  GLY  ILE  ALA ...
T C T A A G A A T G T T T A T T T G A A A G G T A T T G C G...
                2530                2540...

...  THR  THR  LEU  THR  GLU  PRO  SER  ALA  GLY  ALA
... A C A A C T T T A A C T G A G C C A A G C G C G G G A G C G
...                 2560                2570                2580

LYS  SER  SER  HIS  VAL  ASP  LEU  ASN  VAL  ASP ...
A A G T C T T C A C A C G T T G A T T T A A A T G T G G A T...
                2590                2600                2610...

...  ALA  THR  LYS  LYS  SER  ASN  ALA  ALA  SER  ILE
... G C G A C G A A A A A A A T C C A A T G C A G C A A G T A T T
...                 2620                2630                2640

GLU  ASP  VAL  LEU  ARG  ALA  GLY  TRP  ASN  ILE ...
G A A G A T G T A T T G C G C G C A G G T T G G A A T A T T...
                2650                2660                2670...

...  GLN  GLY  ASN  GLY  ASN  ASN  VAL  ASP  TYR  VAL
... C A A G G T A A T G G T A A T A A T G T T G A T T A T G T A
...                 2680                2690                2700

ALA  THR  TYR  ASP  THR  VAL  ASN  PHE  THR  ASP ...
G C G A C G T A T G A C A C A G T T A A A C T T T A C C G A T...
                2710                2720                2730...
```

FIG.24N

```
                                       ... ASP  SER  THR  GLY  THR  THR  THR  VAL  THR  VAL
                                       ... G A C A G C A C A G G T A C A A C A A C G G T A A C C G T A
                                       ...          2740                2750                2760

THR  GLN  LYS  ALA  ASP  GLY  LYS  GLY  ALA  ASP ...
A C C C A A A A A G C A G A T G G C A A A G G T G C T G A C...
           2770                2780                2790...
                                       ... VAL  LYS  ILE  GLY  ALA  LYS  THR  SER  VAL  ILE
                                       ... G T T A A A A T C G G T G C G A A A A C T T C T G T T A T C
                                       ...          2800                2810                2820

LYS  ASP  HIS  ASN  GLY  LYS  LEU  PHE  THR  GLY ...
A A A G A C C A C A A C G G C A A A C T G T T T A C A G G C...
           2830                2840                2850...
                                       ... LYS  ASP  LEU  LYS  ASP  ALA  ASN  ASN  GLY  ALA
                                       ... A A A G A C C T G A A A G A T G C G A A T A A T G G T G C A
                                       ...          2860                2870                2880

THR  VAL  SER  GLU  ASP  ASP  GLY  LYS  ASP  THR ...
A C C G T T A G T G A A G A T G A T G G C A A A G A C A C C...
           2890                2900                2910...
                                       ... GLY  THR  GLY  LEU  VAL  THR  ALA  LYS  THR  VAL
                                       ... G G C A C A G G C T T A G T T A C T G C A A A A A C T G T G
                                       ...          2920                2930                2940
```

FIG.24O

```
ILE  ASP  ALA  VAL  ASN  LYS  SER  GLY  TRP  ARG ...
A T T G A T G C A G T A A A T A A A A G C G G T T G G A G G...
                2950                2970...

...  VAL  THR  GLY  GLU  GLY  ALA  THR  ALA  GLU  THR
... G T A A C C G G T G A G G G C G C G A C T G C C G A A A C C
...                 2980                2990                3000

GLY  ALA  THR  ALA  VAL  ASN  ALA  GLY  ASN  ALA ...
G G T G C A A C C G C C G T G A A T G C G G G T A A C G C T...
                3010                3020...

...  GLU  THR  VAL  THR  SER  GLY  THR  SER  VAL  ASN
... G A A A C C G T T A C A T C A G G C A C G A G C G T G A A C
...                 3040                3050                3060

PHE  LYS  ASN  GLY  ASN  ALA  THR  THR  ALA  THR ...
T T C A A A A A C G G G C A A T G C G A C C A C G C G A C C...
                3070                3080...

...  VAL  SER  LYS  ASP  ASN  GLY  ASN  ILE  ASN  VAL
... G T A A G C A A A G A T A A T G G C A A C A T C A A T G T C
...                 3100                3110                3120

LYS  TYR  ASP  VAL  ASN  VAL  GLY  ASP  GLY  LEU ...
A A A T A C G A T G T A A A T G T T G G T G A C G G C T T G...
                3130                3140                3150...
```

FIG.24P

```
                ... LYS  ILE  GLY  ASP  ASP  LYS  LYS  ILE  VAL  ALA
                ... A A G A T T G G C G A T G A C A A A A A A T C G T T G C A
                ...                3160                3170                3180

ASP  THR  THR  THR  LEU  THR  VAL  THR  GLY  GLY ...
G A C A C G A C C A C A C T T A C T G T A A C A G G T G G T...
                3190                3200                3210...
                ... LYS  VAL  SER  VAL  PRO  ALA  GLY  ALA  ASN  SER
                ... A A G G T G T C T G T T C C T G C T G G T G C T A A T A G T
                ...                3220                3230                3240

VAL  ASN  ASN  ASN  LYS  LYS  LEU  VAL  ASN  ALA ...
G T T A A T A A C A A T A A G A A A C T T G T T A A T G C A...
                3250                3260                3270...
                ... GLU  GLY  LEU  ALA  THR  ALA  LEU  ASN  ASN  LEU
                ... G A G G G T T T A G C G A C T G C T T T A A C A A C C T A
                ...                3280                3290                3300

SER  TRP  THR  ALA  LYS  ALA  ASP  LYS  TYR  ALA ...
A G C T T G G A C G G C A A A A G C C G A T A A A T A T G C A...
                3310                3320                3330...
                ... ASP  GLY  GLU  SER  GLU  GLY  GLU  THR  ASP  GLN
                ... G A T G G C G A G T C A G A G G G C G A A A C C G A C C A A
                ...                3340                3350                3360
```

09/936362

FIG.24Q

```
GLU   VAL   LYS   ALA   GLY   ASP   LYS   VAL   THR   PHE ...
G A A G T C A A A G C A G G C G A C A A A G T A A C C T T T...
              3370                3380                3390...
                                  ... LYS   ALA   GLY   LYS   ASN   LEU   LYS   VAL   LYS   GLN
                                  ... A A A G C A G G C A A G A A C T T A A A A G T G A A A C A G
                                  ...                3400                3410                3420

SER   GLU   LYS   ASP   PHE   THR   TYR   SER   LEU   GLN ...
T C T G A A A A A G A C T T T A C T T A T T C A C T G C A A...
              3430                3440                3450...
                                  ... ASP   THR   LEU   THR   GLY   LEU   THR   SER   ILE   THR
                                  ... G A C A C T T T A A C A G G C T T A A C G A G C A T T A C T
                                  ...                3460                3470                3480

LEU   GLY   GLY   THR   ALA   ASN   GLY   ARG   ASN   ASP ...
T T A G G T G G T A C A G C T A A T G G C A G A A A T G A T...
              3490                3500                3510...
                                  ... THR   GLY   THR   VAL   ILE   ASN   LYS   ASP   GLY   LEU
                                  ... A C G G G A A C C G T C A T C A A C A A A G A C G G C T T A
                                  ...                3520                3530                3540

THR   ILE   THR   LEU   ALA   ASN   GLY   ALA   ALA   ALA ...
A C C A T C A C G C T G G C A A A T G G T G C T G C G G C A...
              3550                3560                3570...
```

FIG.24R

```
                              ... GLY THR ASP ALA SER ASN GLY ASN THR ILE
                              ... G G C A C A G A T G C G T C T A A C G G A A A C A C C A T C
                              ...            3580           3590           3600

SER VAL THR LYS ASP GLY ILE SER ALA GLY ...
A G T G T A A C C A A A G A C G G C A T T A G T G C G G G T...
       3610           3620           3630...
                              ... ASN LYS GLU ILE THR ASN VAL LYS SER ALA
                              ... A A T A A A G A A A T T A C C A A T G T T A A G A G T G C T
                              ...            3640           3650           3660

LEU LYS THR TYR LYS ASP THR GLN ASN THR ...
T T A A A A A C C T A T A A A G A T A C T C A A A A C A C T...
       3670           3680           3690...
                              ... ALA GLY ALA THR GLN PRO ALA ALA ASN THR
                              ... G C A G G T G C A A C T C A A C C T G C G G C T A A T A C A
                              ...            3700           3710           3720

ALA GLU VAL ALA LYS GLN ASP LEU VAL ASP ...
G C T G A A G T A G C C A A A C A A G A C T T G G T T G A T...
       3730           3740           3750...
                              ... LEU THR LYS PRO ALA THR GLY ALA ALA GLY
                              ... T T A A C T A A A C C T G C G A C A G G T G C A G C T G G A
                              ...            3760           3770           3780
```

FIG.24S

```
ASN  GLY  ALA  ASP  ALA  LYS  ALA  PRO  ASP  THR ...
A A T G G T G C A G A T G C A A A A G C T C C C G A T A C C...
                3790                 3800                 3810...

                     ...  THR  ALA  ALA  THR  VAL  GLY  ASP  LEU  ARG  GLY
                     ... A C A G C T G C A A C C G T A G G C G A C T T G C G T G G T
                     ...                  3820                 3830                 3840

LEU  GLY  TRP  VAL  LEU  SER  ALA  LYS  LYS  THR ...
T T G G G C T G G G T G C T T T C A G C T A A G A A A A C T...
                3850                 3860                 3870...

                     ...  ALA  ASP  GLU  THR  GLN  ASP  LYS  GLU  PHE  HIS
                     ... G C A G A T G A A A A C C A C A A G A T A A A G A G T T C C A C
                     ...                  3880                 3890                 3900

ALA  ALA  VAL  LYS  ASN  ALA  ASN  GLU  VAL  GLU ...
G C C G C C G T T A A A A A C G C A A A T G A A G T T G A G...
                3910                 3920                 3930...

                     ...  PHE  VAL  GLY  LYS  ASN  GLY  ALA  THR  VAL  SER
                     ... T T C G T G G G T A A A A A C G G T G C A A C C G T G T C T
                     ...                  3940                 3950                 3960

ALA  LYS  THR  ASP  ASN  ASN  GLY  LYS  HIS  THR ...
G C A A A A A C T G A T A A C A A C G G A A A A C A T A C T...
                3970                 3980                 3990...
```

09/936362

FIG.24T

```
                                ... VAL  THR  ILE  ASP  VAL  ALA  GLU  ALA  LYS  VAL
                                ... G T A A C G A T T G A T G T T G C A G A A G C C A A A G T T
                                ...             4000             4010             4020

GLY  ASP  GLY  LEU  GLU  LYS  ASP  THR  ASP  GLY ...
G G T G A T G G T C T T G A A A A A G A T A C T G A C G G C...
          4030             4040             4050...
                                ... LYS  ILE  LYS  LEU  LYS  VAL  ASP  ASN  THR  ASP
                                ... A A G A T T A A A C T C A A A G T A G A T A A T A C A G A T
                                ...             4060             4070             4080

GLY  ASN  ASN  LEU  LEU  THR  VAL  ASP  ALA  THR ...
G G G A A T A A T C T A T T A A C C G T T G A T G C A A C A...
          4090             4100             4110...
                                ... LYS  GLY  ALA  SER  VAL  ALA  LYS  GLY  GLU  PHE
                                ... A A A G G T G C A T C C G T T G C C A A G G G C G A G T T T
                                ...             4120             4130             4140

ASN  ALA  VAL  THR  THR  ASP  ALA  THR  THR  ALA ...
A A T G C C G T A A C A A C A G A T G C A A C T A C A G C C...
          4150             4160             4170...
                                ... GLN  GLY  THR  ASN  ALA  ASN  GLU  ARG  GLY  LYS
                                ... C A A G G C A C A A A T G C C A A T G A G C G C G G T A A A
                                ...             4180             4190             4200
```

FIG.24U

```
VAL   VAL   VAL   LYS   GLY   SER   ASN   GLY   ALA   THR ...
G T G G T T G T C A A G G G T T C A A A T G G T G C A A C T...
                4210                 4220                 4230...
                                     ... ALA   THR   GLU   THR   ASP   LYS   LYS   LYS   VAL   ALA
                                     ... G C T A C C G A A A C T G A C A A G A A A A A G T G G C A
                                     ...               4240                 4250                 4260

THR   VAL   GLY   ASP   VAL   ALA   LYS   ALA   ILE   ASN ...
A C T G T T G G C G A C G T T G C T A A A G C G A T T A A C...
                4270                 4280                 4290...
                                     ... ASP   ALA   ALA   THR   PHE   VAL   LYS   VAL   GLU   ASN
                                     ... G A C G C A G C A A C T T T C G T G A A A G T G G A A A A T
                                     ...               4300                 4310                 4320

ASP   ASP   SER   ALA   THR   ILE   ASP   ASP   SER   PRO ...
G A C G A C A G T G C T A C G A T T G A T G A T A G C C C A...
                4330                 4340                 4350...
                                     ... THR   ASP   ASP   GLY   ALA   ASN   ASP   ALA   LEU   LYS
                                     ... A C A G A T G A T G G C G C A A A T G A T G C T C T C A A A
                                     ...               4360                 4370                 4380

ALA   GLY   ASP   THR   LEU   THR   LEU   LYS   ALA   GLY ...
G C A G G C G A C A C C T T G A C C T T A A A A G C G G G T...
                4390                 4400                 4410...
```

FIG.24V

```
                                    ... LYS  ASN  LEU  LYS  VAL  LYS  ARG  ASP  GLY  LYS
                                    ... AAAAACTTAAAAGTTAAACGTGATGGTAAA
                                    ...              4420              4430              4440

 ASN  ILE  THR  PHE  ALA  LEU  ALA  ASN  ASP  LEU ...
AATATTACTTTTGCCCTTGCGAACGACCTT...
              4450              4460              4470...
                                    ... SER  VAL  LYS  SER  ALA  THR  VAL  SER  ASP  LYS
                                    ... AGTGTAAAAAGCGCAACCGTTAGCGATAAA
                                    ...              4480              4490              4500

 LEU  SER  LEU  GLY  THR  ASN  GLY  ASN  LYS  VAL ...
TTATCGCTTGGTACAAACGGCAATAAAGTC...
              4510              4520              4530...
                                    ... ASN  ILE  THR  SER  ASP  THR  LYS  GLY  LEU  ASN
                                    ... AATATCACAAGCGACACCAAAGGCTTGAAC
                                    ...              4540              4550              4560

 PHE  ALA  LYS  ASP  SER  LYS  THR  GLY  ASP  ASP ...
TTCGCTAAAGATAGTAAGACAGGCGATGAT...
              4570              4580              4590...
                                    ... ALA  ASN  ILE  HIS  LEU  ASN  GLY  ILE  ALA  SER
                                    ... GCTAATATTCACTTAAATGGCATTGCTTCA
                                    ...              4600              4610              4620
```

FIG.24W

```
 THR  LEU  THR  ASP  THR  LEU  LEU  ASN  SER  GLY ...
ACTTTAACTGATACATTGTTAAATAGTGGT...
          4630          4640          4650...
                ... ALA  THR  THR  ASN  LEU  GLY  GLY  ASN  GLY  ILE
                ...GCGACAACCAATTTAGGTGGTAATGGTATT
                ...           4660          4670          4680

 THR  ASP  ASN  GLU  LYS  LYS  ARG  ALA  ALA  SER ...
ACTGATAACGAGAAAAAACGCGCGGCGAGC...
          4690          4700          4710...
                ... VAL  LYS  ASP  VAL  LEU  ASN  ALA  GLY  TRP  ASN
                ...GTTAAAGATGTCTTGAATGCGGGTTGGAAT
                ...           4720          4730          4740

 VAL  ARG  GLY  VAL  LYS  PRO  ALA  SER  ALA  ASN ...
GTTCGTGGTGTTAAACCGGCATCTGCAAAT...
          4750          4760          4770...
                ... ASN  GLN  VAL  GLU  ASN  ILE  ASP  PHE  VAL  ALA
                ...AATCAAGTGGAGAATATCGACTTTGTAGCA
                ...           4780          4790          4800

 THR  TYR  ASP  THR  VAL  ASP  PHE  VAL  SER  GLY ...
ACCTACGACACAGTGGACTTTGTTAGTGGA...
          4810          4820          4830...
```


09/936362

FIG.24X

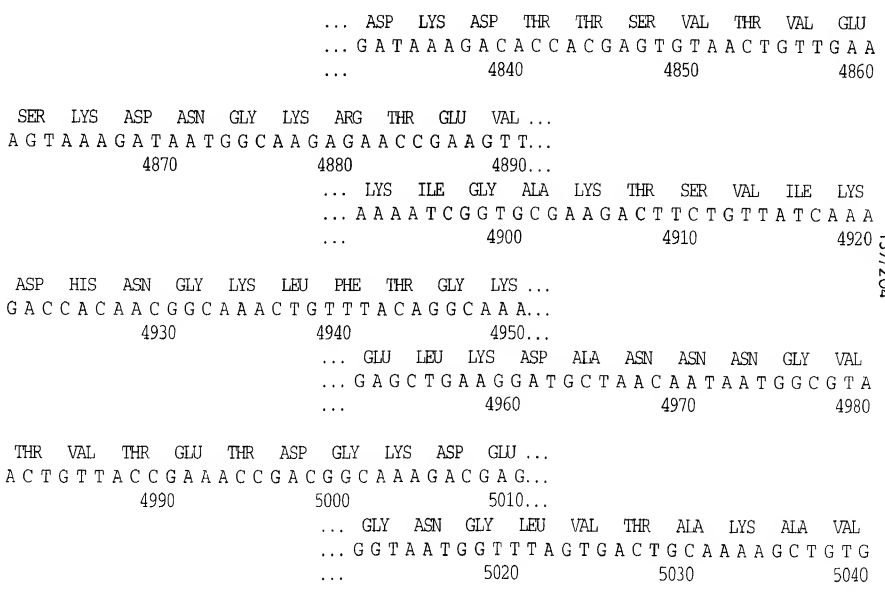


FIG.24Y

```
ILE  ASP  ALA  VAL  ASN  LYS  ALA  GLY  TRP  ARG ...
ATTGATGCCGTGAATAAGGCTGGTTGGAGA...
                5050                5060                5070...

                ...  VAL  LYS  THR  THR  GLY  ALA  ASN  GLY  GLN  ASN
                ... GTTAAAACAACAGGTGCTAATGGTCAGAAT
                ...                 5080                5090                5100

ASP  ASP  PHE  ALA  THR  VAL  ALA  SER  GLY  THR ...
GATGACTTCGCAACTGTTGCGTCAGGCACA...
          5110                5120                5130...

          ...  ASN  VAL  THR  PHE  ALA  ASP  GLY  ASN  GLY  THR
          ... AATGTAACCTTTGCTGATGGTAATGGCACA
          ...                 5140                5150                5160

THR  ALA  GLU  VAL  THR  LYS  ALA  ASN  ASP  GLY ...
ACTGCCGAAGTAACTAAAGCAAACGACGGT...
          5170                5180                5190...

          ...  SER  ILE  THR  VAL  LYS  TYR  ASN  VAL  LYS  VAL
          ... AGTATTACTGTTAAATACAATGTTAAAGTG
          ...                 5200                5210                5220

ALA  ASP  GLY  LEU  LYS  LEU  ASP  GLY  ASP  LYS ...
GCTGATGGCTTAAAACTAGACGGCGATAAA...
          5230                5240                5250...
```

FIG.24Z

```
... ILE  VAL  ALA  ASP  THR  THR  VAL  LEU  THR  VAL
... A T C G T T G C A G A C A C G A C C G T A C T T A C T G T G
...                 5260                 5270                 5280

ALA  ASP  GLY  LYS  VAL  THR  ALA  PRO  ASN  ASN ...
G C A G A T G G T A A A G T T A C A G C T C C G A A T A A T...
                 5290                 5300                 5310...

...  GLY  ASP  GLY  LYS  LYS  PHE  VAL  ASP  ALA  SER
... G G C G A T G G T A A G A A A A T T T G T T G A T G C A A G T
...                 5320                 5330                 5340

GLY  LEU  ALA  ASP  ALA  LEU  ASN  LYS  LEU  SER ...
G G T T T A G C G G A T G C G T T A A A T A A A T T A A G C...
                 5350                 5360                 5370...

...  TRP  THR  ALA  THR  ALA  GLY  LYS  GLU  GLY  THR
... T G G A C G G C A A C T G C T G G T A A A G A A G G C A C T
...                 5380                 5390                 5400

GLY  GLU  VAL  ASP  PRO  ALA  ASN  SER  ALA  GLY ...
G G T G A A G T T G A T C C T G C A A A T T C A G C A G G G...
                 5410                 5420                 5430...

...  GLN  GLU  VAL  LYS  ALA  GLY  ASP  LYS  VAL  THR
... C A A G A A G T C A A A G C G G G C G A C A A A G T A A C C
...                 5440                 5450                 5460
```

09/936362

FIG.24A'

```
PHE LYS ALA GLY ASP ASN LEU LYS ILE LYS ...
T T T A A A G C C G G C G A C A A C C T G A A A A T C A A A...
          5470                5480                5490...
                                ... GLN SER GLY LYS ASP PHE THR TYR SER LEU
                                ... C A A A G C G G C A A A G A C T T T A C C T A C T C G C T G
                                ...             5500                5510                5520

LYS LYS GLU LEU LYS ASP LEU THR SER VAL ...
A A A A A A G A G C T G A A A G A C C T G A C C A G C G T A...
          5530                5540                5550...
                                ... GLU PHE LYS ASP ALA ASN GLY GLY THR GLY
                                ... G A G T T C A A A G A C G C A A A C G G C G G T A C A G G C
                                ...             5560                5570                5580

SER GLU SER THR LYS ILE THR LYS ASP GLY ...
A G T G A A A G C A C C A A G A T T A C C A A A G A C G G C...
          5590                5600                5610...
                                ... LEU THR ILE THR PRO ALA ASN GLY ALA GLY
                                ... T T G A C C A T T A C G C C G G C A A A C G G T G C G G G T
                                ...             5620                5630                5640

ALA ALA GLY ALA ASN THR ALA ASN THR ILE ...
G C G G C A G G T G C A A A C A C T G C A A A C A C C A T T...
          5650                5660                5670...
```

FIG.24B'

```
                                    ... SER  VAL  THR  LYS  ASP  GLY  ILE  SER  ALA  GLY
                                    ... A G C G T A A C C A A A G A T G G C A T T A G C G C G G G T
                                    ...              5680              5690              5700

 ASN  LYS  ALA  VAL  THR  ASN  VAL  VAL  SER  GLY ...
A A T A A A G C A G T T A C A A A C G T T G T G A G C G G A...
               5710              5720              5730...
                                    ... LEU  LYS  LYS  PHE  GLY  ASP  GLY  HIS  THR  LEU
                                    ... C T G A A G A A A T T T G G T G A T G G T C A T A C G T T G
                                    ...              5740              5750              5760

 ALA  ASN  GLY  THR  VAL  ALA  ASP  PHE  GLU  LYS ...
G C A A A T G G C A C T G T T G C T G A T T T T G A A A A G...
               5770              5780              5790...
                                    ... HIS  TYR  ASP  ASN  ALA  TYR  LYS  ASP  LEU  THR
                                    ... C A T T A T G A C A A T G C C T A T A A A G A C T T G A C C
                                    ...              5800              5810              5820

 ASN  LEU  ASP  GLU  LYS  GLY  ALA  ASP  ASN  ASN ...
A A T T T G G A T G A A A A A G G C G C G G A T A A T A A T...
               5830              5840              5850...
                                    ... PRO  THR  VAL  ALA  ASP  ASN  THR  ALA  ALA  THR
                                    ... C C G A C T G T T G C C G A C A A T A C C G C T G C A A C C
                                    ...              5860              5870              5880
```

FIG.24C'

```
VAL  GLY  ASP  LEU  ARG  GLY  LEU  GLY  TRP  VAL ...
G T G G G C G A T T T G C G C G G C T T G G G C T G G T C...
                5890                5900                5910...

LYS  THR  THR  GLY  GLU  PRO
A A A A C C A C A G G C G A A C C C
                5930                5940

ASN  GLN  GLU  TYR  ASN  ALA  GLN  VAL  ARG  ASN ...
A A T C A G G G A A T A C A A C G C G C A A G T G C G T A A C...
                5950                5960                5970...

LYS  PHE  LYS  SER  GLY  ASN
A A A T T C A A G A G C G G C A A C
                5990                6000

GLY  ILE  ASN  VAL  SER  GLY  LYS  THR  LEU  ASN ...
G G T A T C A A T G T T T C C G G T A A A A C A T T G A A C...
                6010                6020                6030...

ILE  THR  PHE  GLU  LEU  ALA
A T T A C C T T T G A A T T G G C T
                6050                6060

LYS  GLY  GLU  VAL  VAL  LYS  SER  ASN  GLU  PHE ...
A A A G G C G A A G T G G T T A A A T C G A A T G A A T T T...
                6070                6080                6090...
```

FIG.24D'

```
... THR VAL LYS ASN ALA ASP GLY SER GLU THR
... A C C G T T A A G A A T G C C G A T G G T T C G G A A A C G
...               6100                6110                6120

ASN LEU VAL LYS VAL GLY ASP MET TYR TYR ...
A A C T T G G T T A A A G T T G G C G A T A T G T A T T A C...
            6130            6140            6150...
... SER LYS GLU ASP ILE ASP PRO ALA THR SER
... A G C A A A G A G G A T A T T G A C C C G G C A A C C A G T
...               6160                6170                6180

LYS PRO MET THR GLY LYS THR GLU LYS TYR ...
A A A C C G A T G A C A G G T A A A A C T G A A A A A T A T...
            6190            6200            6210...
... LYS VAL GLU ASN GLY LYS VAL VAL SER ALA
... A A G G T T G A A A A C G G C A A A G T C G T T T C T G C T
...               6220                6230                6240

ASN GLY SER LYS THR GLU VAL THR LEU THR ...
A A C G G C A G C A A G A C C G A A G T T A C C C T A A C C...
            6250            6260            6270...
... ASN LYS GLY SER GLY TYR VAL THR GLY ASN
... A A C A A A G G T T C C G G C T A T G T A A C A G G T A A C
...               6280                6290                6300
```

09/936362

FIG.24E'

```
GLN  VAL  ALA  ASP  ALA  ILE  ALA  LYS  SER  GLY ...
C A A G T G G C T G A T G C G A A A T C A G G C...
          6310                 6320            6330...

...  PHE  GLU  LEU  GLY  LEU  ALA  ASP  ALA  ALA  GLU
... T T T G A G C T T G G T T T G G C T G A T G C G G C A G A A
...                  6340                 6350            6360

ALA  GLU  LYS  ALA  PHE  ALA  GLU  SER  ALA  LYS ...
G C T G A A A A A G C C T T T G C A G A A G C G C A A A A...
          6370                 6380            6390...

...  ASP  LYS  GLN  LEU  SER  LYS  ASP  LYS  ALA  GLU
... G A C A A G C A A T T G T C T A A A G A T A A A G C G G A A A
...                  6400                 6410            6420

THR  VAL  ASN  ALA  HIS  ASP  LYS  VAL  ARG  PHE ...
A C T G T A A A T G C C C A C G A T A A A G T C C G T T T T...
          6430                 6440            6450...

...  ALA  ASN  GLY  LEU  ASN  THR  LYS  VAL  SER  ALA
... G C T A A T G G T T T A A A T A C C A A A G T G A G C G C G
...                  6460                 6470            6480

ALA  THR  VAL  GLU  SER  THR  ASP  ALA  ASN  GLY ...
G C A A C G G T G G A A A G C A C T G A T G C A A A C G G C...
          6490                 6500            6510...
```

FIG.24F'

```
... ASP LYS VAL THR THR THR PHE VAL LYS THR
... G A T A A A G T G A C C A C A A C C T T G T G A A A A C C
...                6520      6530      6540

ASP VAL GLU LEU PRO LEU THR GLN ILE TYR ...
G A T G T G G A A T T G C C T T T A A C G C A A A T C T A C...
                6550      6560      6570...

... ASN THR ASP ALA ASN GLY ASN LYS ILE VAL
... A A T A C C G A T G C A A A C G G T A A T A A G A T C G T T
...                6580      6590      6600

LYS LYS ALA ASP GLY LYS TRP TYR GLU LEU ...
A A A A A A G C T G A C G G A A A A T G G T A T G A A C T G...
                6610      6620      6630...

... ASN ALA ASP GLY THR ALA SER ASN LYS GLU
... A A T G C T G A T G G T A C G G C G A G T A A C A A A G A A
...                6640      6650      6660

VAL THR LEU GLY ASN VAL ASP ALA ASN GLY ...
G T G A C A C T T G G T A A C G T G G A T G C A A A C G G T...
                6670      6680      6690...

... LYS LYS VAL VAL LYS VAL THR GLU ASN GLY
... A A G A A A G T T G T G A A A G T A A C C G A A A A T G G T
...                6700      6710      6720
```

FIG.24G'

```
ALA ASP LYS TRP TYR TYR THR ASN ALA ASP ...
G C G G A T A A G T G G T A T T A C A C C A A T G C T G A C...
                6730                6740                6750...
                                    ... GLY ALA ALA ASP LYS THR LYS GLY GLU VAL
                                    ... G G T G C T G C G G A T A A A A A C C A A G G C G A A G T G
                                    ...                 6760                6770                6780

SER ASN ASP LYS VAL SER THR ASP GLU LYS ...
A G C A A T G A T A A G T T C T A C C G A T G A A A A A...
                6790                6800                6810...
                                    ... HIS VAL VAL ARG LEU ASP PRO ASN ASN GLN
                                    ... C A C G T T G T C C G C C T T G A T C C G A A C A A T C A A
                                    ...                 6820                6830                6840

SER ASN GLY LYS GLY VAL VAL ILE ASP ASN ...
T C G A A C G G C A A G G C G T G G T C A T T G A C A A T...
                6850                6860                6870...
                                    ... VAL ALA ASN GLY GLU ILE SER ALA THR SER
                                    ... G T G G C T A A T G G C G A A A T T C T G C C A C T T C C
                                    ...                 6880                6890                6900

THR ASP ALA ILE ASN GLY SER GLN LEU TYR ...
A C C G A T G C G A T T A A C G G A A G T C A G T T G T A T...
                6910                6920                6930...
```

FIG.24H'

```
... ALA VAL ALA LYS GLY VAL THR ASN LEU ALA
... G C C G T G G C A A A A G G G G T A A C A A A C C T T G C T
...                6940      6950      6960

GLY GLN VAL ASN ASN LEU GLU GLY LYS VAL ...
G G A C A A G T G A A T A A T C T T G A G G G C A A A G T G...
          6970      6980      6990...

... ASN LYS VAL GLY LYS ARG ALA ASP ALA GLY
... A A T A A A G T G G G C A A A C G T G C A G A T G C A G G T
...                7000      7010      7020

THR ALA SER ALA LEU ALA ALA SER GLN LEU ...
A C A G C A A G T G C A T T A G C G G C T T C A C A G T T A...
          7030      7040      7050...

... PRO GLN ALA THR MET PRO GLY LYS SER MET
... C C A C A A G C C C A C T A T G C C C A G G T A A A T C A A T G
...                7060      7070      7080

VAL ALA ILE ALA GLY SER SER TYR GLN GLY ...
G T T G C T A T T G C G G G A A G T A G T T A T C A A G G T...
          7090      7100      7110...

... GLN ASN GLY LEU ALA ILE GLY VAL SER ARG
... C A A A A T G G T T T A G C T A T C G G G G T A T C A A G A
...                7120      7130      7140
```

FIG.24I'

```
 ILE   SER   ASP   ASN   GLY   LYS   VAL   ILE   ILE   ARG ...
ATTTCCGATAATGGCAAAGTGATTATTCGC...
            7150              7160              7170...
                              ... LEU   SER   GLY   THR   THR   ASN   SER   GLN   GLY   LYS
                              ... TTGTCAGGCACAACCAATAGTCAAGGTAAA
                              ...               7180              7190              7200

 THR   GLY   VAL   ALA   ALA   GLY   VAL   GLY   TYR   GLN ...
ACAGGCGTTGCAGCAGGTGTTGGTTACCAG...
            7210              7220              7230...
                              ... TRP   ***
                              ... TGGTAATAGAATTCCGGATCCGC
                              ...               7240              7250
```

09/936362

FIG.25A

NTHi strain 12 *hia* locus

```
          TYR  TYR  HIS  TRP  ***  PRO  THR  PRO ...
GAATTCTATTACCACTGGTAACCAACACCT ...
          10        20        30 ...
                              ... ALA  ALA  THR  PRO  GLU  THR  ALA  GLN  GLN  ILE
                              ...GCTGCAACGCCAGAAACAGCACAACAAATT
                              ...        40        50        60

HIS  TRP  LEU  HIS  GLN  PHE  THR  LYS  ALA  ARG ...
CACTGGCTACATCAATTTACCAAAGCTCGC ...
          70        80        90 ...
                              ... ILE  GLN  TRP  ARG  LYS  THR  HIS  SER  LEU  PHE
                              ...ATTCAATGGCGCAAAACCCATTCCTTATTC
                              ...       100       110       120

PHE  LYS  GLU  LYS  PRO  ASP  TYR  ALA  PHE  VAL ...
TTTAAAGAAAAACCCGATTATGCCTTTGTG ...
         130       140       150 ...
                              ... LEU  ALA  GLU  ASN  GLY  LYS  VAL  GLN  GLU  ILE
                              ...CTGGCAGAAAACGGCAAAGTGCAAGAAATC
                              ...       160       170       180

LYS  ALA  GLU  TYR  ARG  ARG  ILE  ALA  ASN  GLN ...
AAAGCAGAATATCGCCGCATTGCCAATCAA ...
         190       200       210 ...
```

FIG.25B

```
                                    ... ILE  VAL  GLU  GLU  ALA  MET  ILE  ILE  ALA  ASN
                                    ...A T T G T G G A A G A A G C A A T G A T T A T T G C C A A C
                                    ...            220                 230                 240

ILE  CYS  ALA  ALA  GLN  PHE  LEU  HIS  GLU  GLN ...
A T C T G C G C C G C C C A A T T T T T A C A C G A A C A G ...
          250                 260                 270 ...
                                    ... ALA  LYS  THR  GLY  ILE  PHE  ASN  ALA  HIS  SER
                                    ...G C A A A A A C A G G C A T T T T C A A C G C C C A C A G C
                                    ...            280                 290                 300

GLY  PHE  ASP  LYS  LYS  TYR  LEU  GLU  ASN  ALA ...
                                         _______...
G G T T T T G A T A A A A A A T A C T T A G A A A A T G C G ...
          310                 320                 330 ...
                                    ... HIS  HIS  PHE  LEU  MET  ALA  ASN  LEU  ALA  ASN
                                    ...___________6431.SL (_______________
                                    ...C A C C A T T T C T T A A T G G C A A A T T T A G C C A A T
                                    ...            340                 350                 360

GLU  GLN  ASN  GLN  THR  GLU  LEU  ALA  GLU  ARG ...
G A A C A A A A T C A A A C T G A A C T G G C A G A A C G T ...
          370                 380                 390 ...
                                    ... TYR  SER  VAL  GLU  ASN  LEU  ALA  THR  LEU  ASN
                                    ...T A T T C A G T A G A A A A C T T A G C A A C C T T A A A C
                                    ...            400                 410                 420
```

FIG.25C

```
GLY  TYR  CYS  GLN  MET  ARG  HIS  ASP  ILE  GLU  ...
G G C T A T T G C C A A A T G C G T C A C G A T A T T G A A  ...
                    430                 440                 450  ...

...  PRO  ILE  GLU  SER  ASP  TYR  LEU  GLU  LEU  ARG
...C C C A T C G A A A G C G A T T A T T T A G A A C T G C G T
...                 460                 470                 480

LEU  ARG  ARG  TYR  LEU  THR  PHE  ALA  GLU  PHE  ...
T T A C G C C C G T T A T T T A A C T T T C G C C G A A T T T  ...
                    490                 500                 510  ...

...  LYS  SER  GLU  LEU  ALA  PRO  HIS  PHE  GLY  LEU
...A A A T C A G A A A T T A G C A C C G C A C T T G G T C T T
...                 520                 530                 540

GLY  LEU  GLU  GLY  TYR  ALA  THR  TRP  THR  SER  ...
G G T T T A G A A G G C T A T G C C A C T T G G A C A T C G  ...
                    550                 560                 570  ...

...  PRO  ILE  ARG  LYS  TYR  SER  ASP  MET  VAL  ASN
...C C C A T C C G C A A A T A T T C A G A T A T G G T T A A T
...                 580                 590                 600

HIS  ARG  LEU  ILE  LYS  ALA  VAL  LEU  ALA  LYS  ...
                                                    ...
C A T C G C T T A A T C A A A G C C G T G C T G G C A A A A  ...
                    610                 620                 630  ...
```

FIG.25D

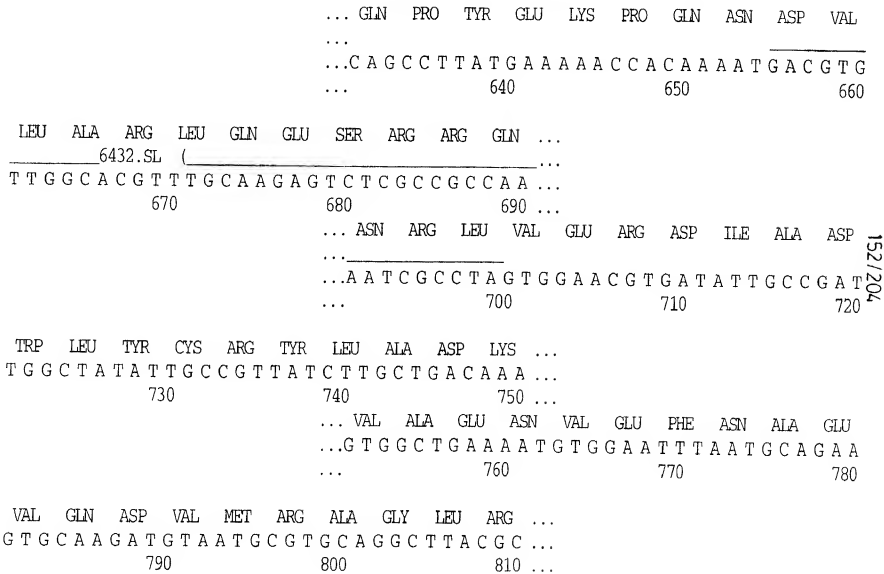


FIG.25E

```
...VAL  GLN  LEU  LEU  GLU  ASN  GLY  ALA  SER  LEU
...G T A C A A C T G C T C G A A A A T G G T G C A T C G C T A
...                820                830                840

PHE  ILE  PRO  ALA  ALA  THR  LEU  HIS  ASN  ASN  ...
T T T A T T C C T G C C G C C A C G T T G C A C A A C A A C  ...
                850                860                870  ...
... LYS  GLU  GLU  ILE  GLN  LEU  ASN  PRO  ASP  GLU
...A A A G A A G A A A T A C A G C T A A A C C C T G A C G A A
...                880                890                900

LEU  ALA  LEU  TYR  ILE  LYS  GLY  GLU  ARG  THR  ...
C T C G C C C T C T A T A T A A A A G G C G A A C G C A C T  ...
                910                920                930  ...
... TYR  LYS  ILE  GLY  ASP  ILE  VAL  LYS  VAL  LYS
...T A C A A A A A T A G G C G A C A T T G T G A A A G T G A A A A
...                940                950                960

LEU  THR  GLU  VAL  LYS  GLU  ALA  THR  ARG  SER  ...
C T C A C T G A A G T G A A A G A A G C A A C T C G C A G T  ...
                970                980                990  ...
... ILE  VAL  GLY  GLU  ILE  LEU  GLN  ***  LEU  PRO
...A T T G T G G G C G A A A T A C T T C A A T A A A T T G C C
...                1000               1010               1020
```

FIG.25F

```
   PHE  GLN  TYR  VAL  THR  GLU  ASP  GLY  LYS  THR...
G T T C C A A T A T G T T A C G G A A G A C G G C A A A A C ...
        1030                 1040                 1050 ...
                ...  VAL  VAL  LYS  VAL  GLY  ASN  GLU  TYR  TYR  GLU
                ...C G T T G T G A A A G T G G G C A A T G A G T A T T A C G A
                ...                  1060                 1070                 1080

   ALA  LYS  GLN  ASP  GLY  SER  ALA  ASP  MET  ASP...
A G C C A A G C A A G A C G G T C G G C G G A T A T G G A ...
                 (  6295.SL
        1090                 1100                 1110 ...
                ...  LYS  LYS  VAL  LYS  ASN  GLY  GLU  LEU  VAL  LYS
                ...T A A A A A A G T C A A A A A T G G C G A G C T G G T G A A A
                ...                  1120                 1130                 1140

   THR  LYS  VAL  LYS  LEU  VAL  SER  ALA  ASN  GLY...
A A C T A A A G T G A A A T T G G T A T C G G C A A A C G G ...
        1150                 1160                 1170 ...
                ...  THR  ASN  PRO  VAL  LYS  ILE  SER  ASN  VAL  ALA
                ...T A C A A A T C C G G T G A A A A T C A G C A A T G T T G C
                ...                  1180                 1190                 1200

   GLU  GLY  THR  GLU  ASP  THR  ASP  ALA  VAL  SER...
G G A A G G G C A C G G A A G A T A C C G A T G C G G T C A G ...
        1210                 1220                 1230 ...
```

FIG.25G

```
... PHE LYS GLN LEU LYS ALA LEU GLN ASN LYS
...C T T T A A G C A G T T G A A A G C C T T G C A A A A C A A
...          1240                 1250                1260

GLN VAL THR LEU SER ALA SER ASN ALA TYR...
A C A G G T T A C G T T A A G C G C G A G C A A T G C T T A ...
          1270                1280               1290 ...

... ALA ASN GLY GLY SER ASP ALA ASP VAL GLY
...T G C C A A T G G C G G T A G C G A T G C C G A C G T C G G
...          1300                 1310                1320

LYS VAL THR GLN THR LEU SER ASN GLY LEU...
C A A G G T A A C T C A A A C T T T A A G C A A T G G T T T ...
          1330                1340               1350 ...

... ASN PHE LYS PHE LYS SER THR ASP GLY GLU
...G A A T T T T A A A T T T A A A T C C A C A G A C G G C G A
...          1360                 1370                1380

LEU LEU ASN ILE LYS ALA ASP LYS ASP THR...
G T T G T T G A A C A T C A A A G C A G A C A A G G A C A C ...
          1390                1400               1410 ...

... VAL THR ILE THR ARG ALA SER GLY ALA ASN
...G G T T A C C A T T A C G C G G G C A A G C G G T G C G A A
...          1420                 1430                1440
```

FIG.25H

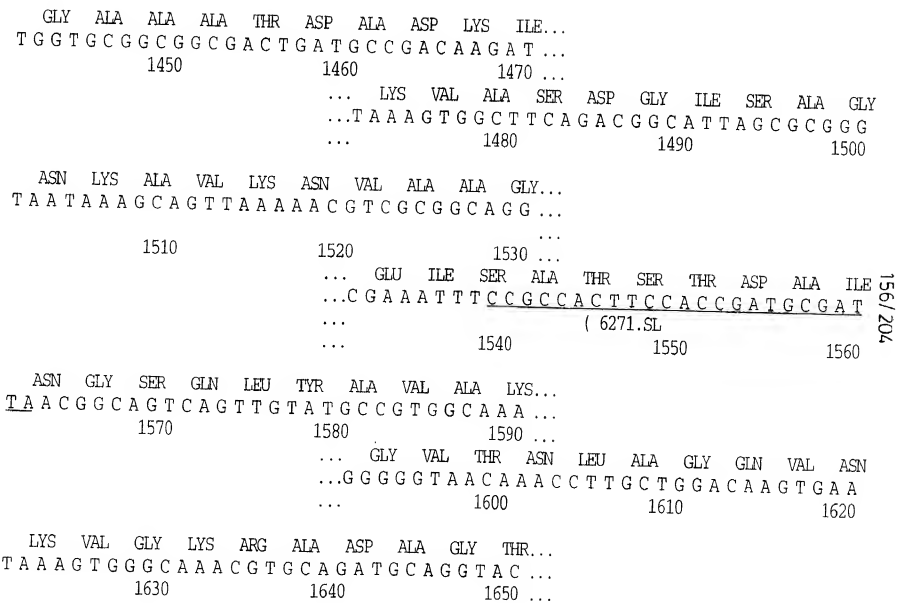


FIG.25I

```
                ...  ALA  SER  ALA  LEU  ALA  ALA  SER  GLN  LEU  PRO
                ...A G C A A G T G C A T T A G C G G C T T C A C A G T T A C C
                ...                1660                1670                1680

      GLN  ALA  SER  MET  PRO  GLY  LYS  SER  MET  VAL...
A C A A G C C C T C T A T G C C C G G G T A A A T C A A T G G T  ...
                1690                1700                1710  ...
                ...  SER  ILE  ALA  GLY  SER  SER  TYR  GLN  GLY  GLN
                ...T T C T A T T G C G G G A A G T A G T T A T C A A G G T C A
                ...                1720                1730                1740

      SER  GLY  LEU  ALA  ILE  GLY  VAL  SER  ARG  ILE...
A A G T G G T T T A G C T A T C G G G G T A T C A A G A A T  ...
                1750                1760                1770  ...
                ...  SER  ASP  ASN  GLY  LYS  LEU  ILE  ILE  ARG  LEU
                ...T T C C G A T A A T G G C A A A T T G A T T A T T C G C T T
                ...                1780                1790                1800

      SER  GLY  THR  THR  ASN  SER  GLN  GLY  LYS  THR...
G T C A G G C A C A A C C A A T A G C C C A A G G T A A A A C  ...
                1810                1820                1830  ...
                ...  GLY  VAL  ALA  ALA  GLY  VAL  GLY  TYR  GLN  TRP
                ...A G G C G T T G C A G C A G G T G T T G G T T A C C A G T G
                ...                1840                1850                1860

***  ***
G T A A T A G A A T T C
                1870
```

FIG.26A

```
ATG AAC AAA ATT TTT AAC GTT ATT TGG AAT GTT GTG ACT CAA ACT TGG      48
Met Asn Lys Ile Phe Asn Val Ile Trp Asn Val Val Thr Gln Thr Trp
        2130                2135                2140

GTT GTC GTA TCT GAA CTC ACT CGC ACC CAC ACC AAA TGC GCC TCC GCC      96
Val Val Val Ser Glu Leu Thr Arg Thr His Thr Lys Cys Ala Ser Ala
        2145                2150                2155

ACC GTG GCG GTT GCC GTA TTG GCA ACC CTG TTG TCC GCA ACG GTT GAG     144
Thr Val Ala Val Ala Val Leu Ala Thr Leu Leu Ser Ala Thr Val Glu
2160                2165                2170                2175

GCG AAC AAC AAT ACT CCT GTT ACG AAT AAG TTG AAG GCT TAT GGC GAT     192
Ala Asn Asn Asn Thr Pro Val Thr Asn Lys Leu Lys Ala Tyr Gly Asp
                2180                2185                2190

GCG AAT TTT AAT TTC ACT AAT AAT TCG ATA GCA GAT GCA GAA AAA CAA     240
Ala Asn Phe Asn Phe Thr Asn Asn Ser Ile Ala Asp Ala Glu Lys Gln
        2195                2200                2205

GTT CAA GAG GCT TAT AAA GGT TTA TTA AAT CTA AAT GAA AAA AAT GCG     288
Val Gln Glu Ala Tyr Lys Gly Leu Leu Asn Leu Asn Glu Lys Asn Ala
        2210                2215                2220
```

FIG.26B

```
AGT GAT AAA CTG TTG GTG GAG GAC AAT ACT GCG GCG ACC GTA GGC AAT      336
Ser Asp Lys Leu Leu Val Glu Asp Asn Thr Ala Ala Thr Val Gly Asn
      2225                2230                2235

TTG CGT AAA TTG GGC TGG GTA TTG TCT AGC AAA AAC GGC ACA AGG AAC      384
Leu Arg Lys Leu Gly Trp Val Leu Ser Ser Lys Asn Gly Thr Arg Asn
      2240                2245                2250                2255

GAG AAA AGC CAA CAA GTC AAA CAT GCG GAT GAA GTG TTG TTT GAA GGC      432
Glu Lys Ser Gln Gln Val Lys His Ala Asp Glu Val Leu Phe Glu Gly
                  2260                2265                2270

AAA GGC CGT GTG CAG GTT ACT TCC ACC TCT GAA AAC GGC AAA CAC ACC      480
Lys Gly Val Gln Val Thr Ser Thr Ser Glu Asn Gly Lys His Thr
            2275                2280                2285

ATT ACC TTT GCT TTA GCG AAA GAC CTT GGT GTG AAA ACT GCG ACT GTG      528
Ile Thr Phe Ala Leu Ala Lys Asp Leu Gly Val Lys Thr Ala Thr Val
      2290                2295                2300

AGT GAT ACC TTA ACG ATT GGC GGT GGT GCT GCA GGT GCT ACA ACA      576
Ser Asp Thr Leu Thr Ile Gly Gly Gly Ala Ala Ala Gly Ala Thr Thr
      2305                2310                2315
```

FIG.26C

```
ACA CCG AAA GTG AAT GTA ACT AGT ACA ACT GAT GGC TTG AAG TTC GCT   624
Thr Pro Lys Val Asn Val Thr Ser Thr Thr Asp Gly Leu Lys Phe Ala
2320                2325                2330                2335

AAA GAT GCT GCG GGT GCT AAT GGC GAT ACT ACG GTT CAC TTG AAT GGT   672
Lys Asp Ala Ala Gly Ala Asn Gly Asp Thr Thr Val His Leu Asn Gly
                    2340                2345                2350

ATT GGT TCA ACC TTG ACA GAC ACG CTT GTG GGT TCT CCT GCT ACT CAT   720
Ile Gly Ser Thr Leu Thr Asp Thr Leu Val Gly Ser Pro Ala Thr His
                2355                2360                2365

ATT GAC GGA GGA GAT CAA AGT ACG CAT TAC ACT CGT GCA GCA AGT ATC   768
Ile Asp Gly Gly Asp Gln Ser Thr His Tyr Thr Arg Ala Ala Ser Ile
            2370                2375                2380

AAG GAT GTC TTG AAT GCG GGT TGG AAT ATC AAG GGT GTT AAA GCT GGC   816
Lys Asp Val Leu Asn Ala Gly Trp Asn Ile Lys Gly Val Lys Ala Gly
        2385                2390                2395

TCA ACA ACT GGT CAA TCA GAA AAT GTC GAT TTT GTT CAT ACT TAC GAT   864
Ser Thr Thr Gly Gln Ser Glu Asn Val Asp Phe Val His Thr Tyr Asp
2400                2405                2410                2415
```

FIG.26D

```
ACT GTT GAG TTC TTG AGT GCG GAT ACA GAG ACC ACG ACT GTT ACT GTA      912
Thr Val Glu Phe Leu Ser Ala Asp Thr Glu Thr Thr Thr Val Thr Val
            2420                2425                2430

GAT AGC AAA GAA AAC GGT AAG AGA ACC GAA GTT AAA ATC GGT GCG AAG      960
Asp Ser Lys Glu Asn Gly Lys Arg Thr Glu Val Lys Ile Gly Ala Lys
            2435                2440                2445

ACT TCT GTT ATC AAA GAA AAA GAC GGT AAG TTA TTT ACT GGA AAA GCT     1008
Thr Ser Val Ile Lys Glu Lys Asp Gly Lys Leu Phe Thr Gly Lys Ala
            2450                2455                2460

AAC AAA GAG ACA AAT AAA GTT GAT GGT GCT AAC GCG ACT GAA GAT GCA     1056
Asn Lys Glu Thr Asn Lys Val Asp Gly Ala Asn Ala Thr Glu Asp Ala
            2465                2470                2475

GAC GAA GGC AAA GGC TTA GTG ACT GCG AAA GAT GTG ATT GAC GCA GTG     1104
Asp Glu Gly Lys Gly Leu Val Thr Ala Lys Asp Val Ile Asp Ala Val
            2480                2485                2490                2495

AAT AAG ACT GGT TGG AGA ATT AAA ACA ACC GAT GCT AAT GGT CAA AAT     1152
Asn Lys Thr Gly Trp Arg Ile Lys Thr Thr Asp Ala Asn Gly Gln Asn
            2500                2505                2510
```

FIG.26E

```
GGC GAC TTC GCA ACT GTT GCA TCA GGC ACA AAT GTA ACC TTT GCT AGT      1200
Gly Asp Phe Ala Thr Val Ala Ser Gly Thr Asn Val Thr Phe Ala Ser
                2515                2520                2525

GGT AAT GGT ACA ACT GCG ACT GTA ACT AAT GGC ACC GAT GGT ATT ACC      1248
Gly Asn Gly Thr Thr Ala Thr Val Thr Asn Gly Thr Asp Gly Ile Thr
            2530                2535                2540

GTT AAG TAT GAT GCG AAA GTT GGC GAC GGC TTA AAA CTA GAT GGC GAT      1296
Val Lys Tyr Asp Ala Lys Val Gly Asp Gly Leu Lys Leu Asp Gly Asp
        2545                2550                2555

AAA ATC GCT GCA GAT ACG ACC GCA CTT ACT GTG AAT GAT GGT AAG AAC      1344
Lys Ile Ala Ala Asp Thr Thr Ala Leu Thr Val Asn Asp Gly Lys Asn
    2560                2565                2570                2575

GCT AAT AAT CCG AAA GGT AAA GTG GCT GAT GTT GCT TCA ACT GAC GAG      1392
Ala Asn Asn Pro Lys Gly Lys Val Ala Asp Val Ala Ser Thr Asp Glu
                2580                2585                2590

AAG AAA TTG GTT ACA GCA AAA GGT TTA GTA ACA GCC TTA AAC AGT CTA      1440
Lys Lys Leu Val Thr Ala Lys Gly Leu Val Thr Ala Leu Asn Ser Leu
            2595                2600                2605
```

FIG.26F

```
AGC TGG ACT ACA ACT GCT GCT GAG GCG GAC GGT GGT ACG CTT GAT GGA      1488
Ser Trp Thr Thr Thr Ala Ala Glu Ala Asp Gly Gly Thr Leu Asp Gly
        2610                2615                2620

AAT GCA AGT GAG CAA GAA GTT AAA GCG GGC GAT AAA GTA ACC TTT AAA      1536
Asn Ala Ser Glu Gln Glu Val Lys Ala Gly Asp Lys Val Thr Phe Lys
        2625                2630                2635

GCA GGC AAG AAC TTA AAA GTG AAA CAA GAG GGT GCG AAC TTT ACT TAT      1584
Ala Gly Lys Asn Leu Lys Val Lys Gln Glu Gly Ala Asn Phe Thr Tyr
2640                2645                2650                2655

TCA CTG CAA GAT GCT TTA ACA GGC TTA ACG AGC ATT ACT TTA GGT ACA      1632
Ser Leu Gln Asp Ala Leu Thr Gly Leu Thr Ser Ile Thr Leu Gly Thr
                2660                2665                2670

GGA AAT AAT GGT GCG AAA ACT GAA ATC AAC AAA GAC GGC TTA ACC ATC      1680
Gly Asn Asn Gly Ala Lys Thr Glu Ile Asn Lys Asp Gly Leu Thr Ile
        2675                2680                2685

ACA CCA GCA AAT GGT GCG GGT GCA AAT AAT GCA AAC ACC ATC AGC GTA      1728
Thr Pro Ala Asn Gly Ala Gly Ala Asn Asn Ala Asn Thr Ile Ser Val
        2690                2695                2700
```

FIG.26G

```
ACC AAA GAC GGC ATT AGT GCG GGC GGT CAG TCG GTT AAA AAC GTT GTG   1776
Thr Lys Asp Gly Ile Ser Ala Gly Gly Gln Ser Val Lys Asn Val Val
    2705                2710                2715

AGC GGA CTG AAG AAA TTT GGT GAT GCG AAT TTC GAT CCG CTG ACT AGC   1824
Ser Gly Leu Lys Lys Phe Gly Asp Ala Asn Phe Asp Pro Leu Thr Ser
2720                2725                2730                2735

TCC GCC GAC AAC TTA ACG AAA CAA AAT GAC GAT GCC TAT AAA GGC TTG   1872
Ser Ala Asp Asn Leu Thr Lys Gln Asn Asp Asp Ala Tyr Lys Gly Leu
                2740                2745                2750

ACC AAT TTG GAT GAA AAA GGT ACA GAC AAG CAA ACT CCA GTT GTT GCC   1920
Thr Asn Leu Asp Glu Lys Gly Thr Asp Lys Gln Thr Pro Val Val Ala
            2755                2760                2765

GAC AAT ACC GCC GCA ACC GTG GGC GAT TTG CGC GGC TTG GGC TGG GTC   1968
Asp Asn Thr Ala Ala Thr Val Gly Asp Leu Arg Gly Leu Gly Trp Val
        2770                2775                2780

ATT TCT GCG GAC AAA ACC ACA GGC GGC TCA ACG GAA TAT CAC GAT CAA   2016
Ile Ser Ala Asp Lys Thr Thr Gly Gly Ser Thr Glu Tyr His Asp Gln
    2785                2790                2795
```

FIG.26H

```
GTT CGG AAT GCG AAC GAA GTG AAA TTC AAA AGC GGC AAC GGT ATC AAT     2064
Val Arg Asn Ala Asn Glu Val Lys Phe Lys Ser Gly Asn Gly Ile Asn
2800                2805                2810                2815

GTT TCC GGT AAA ACG GTC AAC GGT AGG CGT GAA ATT ACT TTT GAA TTG     2112
Val Ser Gly Lys Thr Val Asn Gly Arg Arg Glu Ile Thr Phe Glu Leu
                    2820                2825                2830

GCT AAA GGT GAA GTG GTT AAA TCG AAT GAA TTT ACC GTC AAA GAA ACC     2160
Ala Lys Gly Glu Val Val Lys Ser Asn Glu Phe Thr Val Lys Glu Thr
            2835                2840                2845

AAT GGA AAG GAA ACG AGC CTG GTT AAA GTT GGC GAT AAA TAT TAC AGC     2208
Asn Gly Lys Glu Thr Ser Leu Val Lys Val Gly Asp Lys Tyr Tyr Ser
        2850                2855                2860

AAA GAG GAT ATT GAC TTA ACA ACA GGT CAG CCT AAA TTA AAA GAT GGC     2256
Lys Glu Asp Ile Asp Leu Thr Thr Gly Gln Pro Lys Leu Lys Asp Gly
    2865                2870                2875

AAT ACA GTT GCT GCG AAA TAT CAA GAT AAA GGT GGC AAA GTC GTT TCT     2304
Asn Thr Val Ala Ala Lys Tyr Gln Asp Lys Gly Gly Lys Val Val Ser
2880                2885                2890                2895
```

FIG.26I

```
GTA ACG GAT AAT ACT GAA GCT ACC ATA ACC AAC AAA GGT TCT GGC TAT   2352
Val Thr Asp Asn Thr Glu Ala Thr Ile Thr Asn Lys Gly Ser Gly Tyr
                2900                2905                2910

GTA ACA GGT AAC CAA GTG GCA GAT GCG ATT GCG AAA TCA GGC TTT GAG   2400
Val Thr Gly Asn Gln Val Ala Asp Ala Ile Ala Lys Ser Gly Phe Glu
            2915                2920                2925

CTT GGC TTG GCT GAT GAA GCT GAT GCG AAA CGG GCG TTT GAT GAT AAG   2448
Leu Gly Leu Ala Asp Glu Ala Asp Ala Lys Arg Ala Phe Asp Asp Lys
        2930                2935                2940

ACA AAA GCC TTA TCT GCT GGT ACA ACG GAA ATT GTA AAT GCC CAC GAT   2496
Thr Lys Ala Leu Ser Ala Gly Thr Thr Glu Ile Val Asn Ala His Asp
    2945                2950                2955

AAA GTC CGT TTT GCT AAT GGT TTA AAT ACC AAA GTG AGC GCG GCA ACG   2544
Lys Val Arg Phe Ala Asn Gly Leu Asn Thr Lys Val Ser Ala Ala Thr
2960                2965                2970                2975

GTG GAA AGC ACC GAT GCA AAC GGC GAT AAA GTG ACC ACA ACC TTT GTG   2592
Val Glu Ser Thr Asp Ala Asn Gly Asp Lys Val Thr Thr Thr Phe Val
                2980                2985                2990
```

FIG.26J

```
AAA ACC GAT GTG GAA TTG CCT TTA ACG CAA ATC TAC AAT ACC GAT GCA      2640
Lys Thr Asp Val Glu Leu Pro Leu Thr Gln Ile Tyr Asn Thr Asp Ala
            2995                3000                3005

AAC GGT AAG AAA ATC ACT AAA GTT GTC AAA GAT GGG CAA ACT AAA TGG      2688
Asn Gly Lys Lys Ile Thr Lys Val Val Lys Asp Gly Gln Thr Lys Trp
        3010                3015                3020

TAT GAA CTG AAT GCT GAC GGT ACG GCT GAT ATG ACC AAA GAA GTT ACC      2736
Tyr Glu Leu Asn Ala Asp Gly Thr Ala Asp Met Thr Lys Glu Val Thr
    3025                3030                3035

CTC GGT AAC GTG GAT TCA GAC GGC AAG AAA GTT GTG AAA GAC AAC GAT      2784
Leu Gly Asn Val Asp Ser Asp Gly Lys Lys Val Val Lys Asp Asn Asp
3040                3045                3050                3055

GGC AAG TGG TAT CAC GCC AAA GCT GAC GGT ACT GCG GAT AAA ACC AAA      2832
Gly Lys Trp Tyr His Ala Lys Ala Asp Gly Thr Ala Asp Lys Thr Lys
                3060                3065                3070

GGC GAA GTG AGC AAT GAT AAA GTT TCT ACC GAT GAA AAA CAC GTT GTC      2880
Gly Glu Val Ser Asn Asp Lys Val Ser Thr Asp Glu Lys His Val Val
            3075                3080                3085
```

FIG.26K

```
AGC CTT GAT CCA AAT GAT CAA TCA AAA GGT AAA GGT GTC GTG ATT GAC   2928
Ser Leu Asp Pro Asn Asp Gln Ser Lys Gly Lys Gly Val Val Ile Asp
        3090                3095                3100

AAT GTG GCT AAT GGC GAT ATT TCT GCC ACT TCC ACC GAT GCG ATT AAC   2976
Asn Val Ala Asn Gly Asp Ile Ser Ala Thr Ser Thr Asp Ala Ile Asn
    3105                3110                3115

GGA AGT CAG TTG TAT GCT GTG GCA AAA GGG GTA ACA AAC CTT GCT GGA   3024
Gly Ser Gln Leu Tyr Ala Val Ala Lys Gly Val Thr Asn Leu Ala Gly
3120                3125                3130                3135

CAA GTG AAT AAT CTT GAG GGC AAA GTG AAT AAA GTG GGC AAA CGT GCA   3072
Gln Val Asn Asn Leu Glu Gly Lys Val Asn Lys Val Gly Lys Arg Ala
                3140                3145                3150

GAT GCA GGT ACA GCA AGT GCA TTA GCG GCT TCA CAG TTA CCA CAA GCC   3120
Asp Ala Gly Thr Ala Ser Ala Leu Ala Ala Ser Gln Leu Pro Gln Ala
            3155                3160                3165

ACT ATG CCA GGT AAA TCA ATG GTT GCT ATT GCG GGA AGT AGT TAT CAA   3168
Thr Met Pro Gly Lys Ser Met Val Ala Ile Ala Gly Ser Ser Tyr Gln
        3170                3175                3180
```

FIG.26L

```
GGT CAA AAT GGT TTA GCT ATC GGG GTA TCA AGA ATT TCC GAT AAT GGC   3216
Gly Gln Asn Gly Leu Ala Ile Gly Val Ser Arg Ile Ser Asp Asn Gly
    3185                3190                3195

AAA GTG ATT ATT CGC TTG TCA GGC ACA ACC AAT AGT CAA GGT AAA ACA   3264
Lys Val Ile Ile Arg Leu Ser Gly Thr Thr Asn Ser Gln Gly Lys Thr
3200                3205                3210                3215

GGC GTT GCA GCA GGT GTT GGT TAC CAG TGG                          3294
Gly Val Ala Ala Gly Val Gly Tyr Gln Trp
            3220                3225
```

FIG.27A

Alignment of NTHi strain 12 5' ORF with HI1733 from H. influenzae strain Rd

```
X        10        20        30        40        50        60        70
PTPAATPETAQQIHWLHQFTKARIQWRKTHSLFFKEKPDYAFVLAENGKVQEIKAEYRRIANQIVEEAMIIA
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
AWQPEMPETAQQIHWLHQFTKARIQWRKTHSLFFKEKPDYAFVLAENGKVQEIKAEYRRIANQIVEEAMIIA
330       340       350       360       370       380       390       400

         80        90       100       110       120       130       140
NICAAQFLHEQAKTGIFNAHSGFDKKYLENAHHFLMANLANEQNQTELAERYSVENLATLNGYCQMRHDIEP
 |||||||||||||||| ||||||| ||||| ||||||||||||||||||||||||||||||||||||||||
NICAAQFLHEQAKTGIFNVHSGFDKKFLENAHNFLMANLANEQNQTELAERYSVENLATLNGYCQMRHDIEP
         410       420       430       440       450       460       470

       150       160       170       180       190       200       210
IESDYLELRLRRYLTFAEFKSELAPHFGLGLEGYATWTSPIRKYSDMVNHRLIKAVLAKQPYEKPQNDVLAR
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
IESDYLELRLRRYLTFAEFKSELAPHFGLGLEGYATWTSPIRKYSDMVNHRLIKAVLAKQPYEKPQNDVLAR
       480       490       500       510       520       530       540

     220       230       240       250       260       270       280
LQESRRQNRLVERDIADWLYCRYLADKVAENVEFNAEVQDVMRAGLRVQLLENGASLFIPAATLHNNKEEIQ
 ||| |||||||||||||||||||||| | || ||||||||||||||||||||||||||||||||||||||||
LQEARRQNRLVERDIADWLYCRYLADKVASNAEFEAEVQDVMRAGLRVQLLENGASLFIPAATLHNNKEEIQ
     550       560       570       580       590       600       610
```

FIG.27B

```
290         300         310         320         330
 LNPDELALYIKGERTYKIGDIVKVKLITEVKEATRSIVGEILQ
 ||||||||||||||||||| |||||||||||||||||||||||
 LNPDELALYIKGERTYKIGDMVKVKLITEVKEATRSIVGEILQ
 620         630         640         650         X
```

```
;       ##cross-references GB:L42023; TIGR:HI1733
;       ##note          named as homolog to a protein from Escherichia coli
; SUMMARY          #length 659  #molecular-weight 75782  #checksum 8365

A64139
MFQDNPLLAQLKQQIHDSKEQVEGVVKSTDKAYGFLECDKKTYFIAPPSMKKVMHGDKIKATIEKQGDKE
QAEPEALIEPMLTRFIAKVRFNKDKKLQVLVDHPSINQPIGAQQAKSVKEELQEGDWVVANLKTHPLRDD
RFFYATINQLICRADDELAPWWVILARHEQSRYPVRGAEPYEMLDQKTRENLTALHFVTIDSESIMDMDD
ALYIEPIAQNSTQTGMKLVVAIADPTAYIALDSQIEQEAKQRCFTNYLPGFNIPMLPRELSDELCSLIAN
EIRPALVCYIETDLTGNITAKPHFVSAYVQSKAKLAYNKVSDYLEQADNAWQPEMPETAQQIHWLHQFTK
ARIQWRKTHSLFFKEKPDYAFVLAENGKVQEIKAEYRRIANQIVEEAMLIANICAAQFLHEQAKTGIFNT
HSGFDKKFLENAHNFIMANLANEQNQTELAERYSVENLATLNGYCQMRHDIEPIESDYLELRLRRYLTFA
EFKSELAPHFGLGLEGYAIWISPIRKYSDMVNHRLIKAVLAKQPYEKPQNDVLARLQEARRQNRLVERDI
ADWLYCRYLADKVASNAEFEAEVQDVMRAGLRVQLLENGASLFIPAATLHNNKEEIQLNPDELALYIKGE
RTYKIGDMVKVKLITEVKEATRSIVGEILQ
```

09/936362

FIG.28A

Alignment of *H. influenzae* Hia/Hsf and *M. catarrhalis* 200 kDa proteins

```
               10        20        30        40        50           ...
MNKIFNVIWNVMTQTWAVVSELTRAHTKRASATVAAAVLATVLSATVQA-S-----------...
...........V....V.......T...C......V.....L.......N------------...
...........V....V...........C......V.....A....AE.NN-----------...
...........V....V...........C......V.....A....AE.NN-----------...
...................................T.....L..T....TT-----------...
...........V....V.......T...C......V.....L.....E.NN-----------...
...................................T.....Q....AE.NS-----------...
.....N..........V.......T.........ET.....L.F.....NATDEDEELDPVV...
................V.......T.........ET.....L.F.....NATDEDEELDPVV...
.....K.....V....V............T.....T.............IN---------DA...
..H.YK..F.KA.G.FMA.A.YAKS.STGGGSCATGQ.GSVCTLSFARIAALAVLVIGATLS...
..H.YK..F.KA.G.FMA.A.CAKS.SGGSSSSTAGQ.GSSPVIRLTRVATLAILVIGATLN...
** ** ****  * **  *** *****  ***  *  * *                      ...

...
...----------------------------------------------      33
...----------------------------------------------      32
...----------------------------------------------      29
...----------------------------------------------      K22
...----------------------------------------------      M4071
...----------------------------------------------      11
...----------------------------------------------      K9
...RTAPVLSFHSDKEGTGEKEVTENSNWGIYFDNKGVLKA--------      HSF
```

FIG.28B

```
                    ...RTAPVLSFHSDKEGTGEKEVTENSNWGIYFHNKGVLKA--------   API
                    ...GTFVKVQSTEDDIEDSAATKDDNKNQALKAGDTLTLKA--------   Rd
                    ...GSAYAQKKDTKHIAIGEQNQPRRSGTAKADGDRAIAIGENANAQGG   4223
                    ...GSAYAQN-NSK-AIFGTTGNNDN---ASASNEASIAIGSLAKAHAN   LES-1
                    ...         *      *           *     *     *

--------------------------------------------------------------...
--------------------------------------------------------------...
--------------------------------------------------------------...
--------------------------------------------------------------...
--------------------------------------------------------------...
--------------------------------------------------------------...
--------------------------------------------------------------...
GAITLKAGDNLKIKQNTDESTNASSFTYSLKKDLTDLTSVATEKLSFGANGDKVDITSDANG...
GAITLKAGDNLKIKQ----STNASSFTYSLKKDLTDLTSVATEKLSFGANGDKVDITSDANG...
GKN-LKAKLDQGGKSVTFALAKDLDVKTAKVSDTLTIGGNTPAAGGATP---KVSITSTADG...
QAIAIGSSNKTVNG-SSLDKIGTDITGQESIAIGGDVKASGDASIAIGSDDLHLLDQHGNPK...
QAIAIGGSKPDPRNQAANQKAGSHAKGKESIAIGGDVLAEGDASIAIGSDDLYLDRNSTNSK...
  **          *                   * * * *  * * *   *           ...
                   ...---------------------------------------------   33
                   ...---------------------------------------------   32
                   ...---------------------------------------------   29
                   ...---------------------------------------------   K22
                   ...---------------------------------------------   M4071
                   ...---------------------------------------------   11
```

FIG.28C

```
...-----------------------------------------------   K9
...LKLAKTGNGN--VHLNGLDSTLPDAVTNIGVLSSSS-FTPNDVEKTR   HSF
...LKLAKTGNGN--VHLNGLDSTLPDAVTNIGVLSSSS-FTPNDVEKTR   API
...LKLAKGTNGDTAVHLNGLASTLPDVTTNIGASTSVT-FSPSDIEKTR   Rd
...HPKGTLINDLINGHAVLKEIRSSKDNDVKYRRTTASGHASTAVGAMS   4223
...YPNGLLSTLIQN-HTVLRQIRDSNGSQ-KYRRTAAEGHASTAVGAMA   LES-1
...   *         *                  **   **   *

--------------------------------------------------------------...
--------------------------------------------------------------...
--------------------------------------------------------------...
--------------------------------------------------------------...
--------------------------------------------------------------...
--------------------------------------------------------------...
--------------------------------------------------------------...
AATVKDVLNAGWNIKGAKTAGGNVESVDLVSAYNNVEFITGDKNTLDVVLTAKENGKTTEVK ...
AATVKDVLNAGWNIKGAKTAGGNVESVDLVSAYNNVEFITGDKNTLDVVLTAKENGKTTEVK...
AATIKDVLNAGWNIKGAKVAGGNTESVDLVAGYDNVEFITGDKNTLDVVLTAKENGKTTEVK...
YAQGHFSNAFGTRA-TAKSAYSLAVGLAATAEGQSTIAIGSDATSSSLGAIALGAGTRAQLQ...
YAKGHFANAFGTRS-TAEGNYSKAVGLTAKAEKGYTIAIGSNAQAINYGALALGADTRVDLD...
 *        *   ***    *    *   *       ****  *      *       ** ...

...-----------------------------------------------   33
...-----------------------------------------------   32
...-----------------------------------------------   29
...-----------------------------------------------   K22
```

09/936362

FIG.28D

```
...----------------------------------------------   M4071
...----------------------------------------------   11
...----------------------------------------------   K9
...FTPKT---SVIKEKD----GKLFTGKENNDINKV--TSNTA--------   HSF
...FTPKT---SVIKEKD----GKLFTGKENNDINKV--TSNTA--------   API
...FTPKT---SVIKDNN----GKLLTGKQLKDANTG--TATNA--------   Rd
...GSIALGQGSVVTQSD-NNSRPAYTPNTQALDPKFQ-ATNNTKAGPLSIG   4223
...YGIALGYGSQILNNNNNNNNKAYVPEGNGSNIKSSKATGNGLF---SIG   LES-1
...  *      * * * *                          **  *

---------------------------------------------------------...
---------------------------------------------------------...
---------------------------------------------------------...
---------------------------------------------------------...
---------------------------------------------------------...
---------------------------------------------------------...
---------------------------------------------------------...
TDNTDEGNGLVTAKAVI-DAVNKAGWTVKTTTANGQNGDFATVASGTNVTFESGDGTTASVT...
TDNTDEGNGLVTAKAVI-DAVNKAGWTVKTTTANGQNGDFATVASGTNVTFESGDGTTASVT...
TEDTDEAMA*                                                    ...
 *RYRRGNGLVTAKTVI-EAVNKSGWRVKTTTANGQNDDFATVASGTNVTFANGNGTTASVT...
SNSIKRKIINVGAGVNKTDAVNVAQLEAVVKWAKERRITFQGDDNSTDVKIGLDNTLTIKGG...
SSTIKRKIINVGAGYEDTDAVNVAQLKAVENLAK-RQITFKGDDNGTGVKKKLGETLTIKGG...
*         ***     **** *        *      * *   ** *      ** *   *...

...----------------------------------------          33
```

FIG.28E

```
...------------------------------------------------------------  32
...------------------------------------------------------------  29
...------------------------------------------------------------  K22
...------------------------------------------------------------  M4071
...------------------------------------------------------------  11
...------------------------------------------------------------  K9
...------------------------------------------------------------  HSF
...KDTMANGLTVKYD-ALMGDGLKFDSDKKIVADTTALTVTG---                   Rd
...KDTMANGLTVKYD-ALMGDGLKFDSDKKIVADTTALTVTG---                   API
...                                                              Rd
...NSTD--GTTVKYE-ALMGDGLKIDSDQKIVADTTALTVTG---                   Rd
...AETNA--LTTNNN- IGVVKFALDNSGLKVKLAKTLNNLTEVTTTL                4223
...-ETQADKLTTNNNNIGVVTD-NNTGLKVKLAKNLSGLETVSTKNL                LES-1
   ****** ** * * * * **      *

------------------------------------------------------------...
------------------------------------------------------------...
------------------------------------------------------------...
------------------------------------------------------------...
------------------------------------------------------------...
------------------------------------------------------------...
------------------------------------------------------------...
GKVAETAKEDDKKKLVNAGDLVTALGNLSWKAKAEADTD--GALEGISKDQEVKAGETVTFK...
GKVAETAKEDDKKKLVNAGDLVTALGNLSWKAKAEADTDTDGALEGISKDQEVKAGETVTFK...
GKVAETAKEDDKKKLVNAGDLVTALGNLSWKAKAEADTD--GALEGTSKDQEVKAGETVTFK...
NATTTVKVGSSSSSTTAELLSDSLTTFTQPNTCSQSTSKTVYGVNGVKPTNNAETTPAAIGTT-R...
```

FIG.28F

```
TASEKVTVGSGNN-TAELQSGGLTFT-PTTNA-STDKTVYGTDGLKFTDNSN-TALEDTT-R...
     *        *       * **    * *    *  *     * * *   *     * *...
                                ...----------------------------------   33
                                ...----------------------------------   32
                                ...----------------------------------   29
                                ...----------------------------------   K22
                                ...----------------------------------   M4071
                                ...----------------------------------   11
                                ...----------------------------------   K9
                                ...AGKNLKVKQDGANFTYSLQDALTGLTSATLGGTTNGGNDA   HSF
                                ...AGKNLKVKQDGANFTYSLQDALTGLTSATLGGTTNGGNDA   API
                                ...AGKNLKVKQDGANFTYSLQDALTGLTSATLGGTTNGGNDA   Rd
                                ...ITRDKIGFARD-GDVDE---------------------   4223
                                ...ITKDKIGFSNKAGTVDENKPYLDKDKLKVGNSTLNNGGLT   LES-1
                                ... ***       *         *        ** * *  *

                                     60          70          ...
 ------------------------------AGSTTGTNSLNVYGK-NNSNFNSANNSIA...
 ----------------------------------------------------------...
 ------------------------------NN--.SV..G..A..D---T...TT.......
 ------------------------------N--.SV..G..A..D---T...TT.......
 ------------------------------T.G..S..G.KA..ST..P...A.G..AT...
 ------------------------------N--.PV..K.KA..D-A.F..--T........
 --------------------------------.ASV.CR.....D-T.TK..A.........
KTVINKDGLTITPAGNGGTTGTNTISBTKDGIK..NKAI..VASGLRAYDDA..DVL...AT...
```

FIG.28G

```
KTVINKDGLTITPAGNGGTTGTNTISBTKDGIK..NKAI..VASGLRAYDDA..DVL...AT...
KTVINKDGLTITPAGNGGTTGTNTISBTKDGIK..NKAI..VASGLRAYDDA..DVL...AT...
------------------------------------------------------------...
-------------VNNTIGGSNKQIQVGADGIKFADVNVNVSNAAKFGTTRITEEEIGFAD....
               ** ***   * ** **** *                      * *...

...80        90        100       110       120
...DLNKQNDSVYDGLLNLNEKGTDKSKFLVADETTATVGNLRKL------   33
...---------------------ATDENED..EELEPVQRSV.------   32
.....E.HVQDA.K........D.N..S.....N.A.........------   29
.....E.HVQDA.K........D.N..S.....N.A.........------   K22
.....AR.F.GA..........DAN.N-L..T.DKA.........------   M4071
....AE..VQEA.K........NAS-D.L..E.N.A....D....------   11
..........G.H........N.AN.-.L..D.N.A....D....------   K9
......RHVEDA.K........NAN.QP-..T.S.A....D....------   HSF
......RHVEDA.K........NAN.QP-..TDS.A....D....------   API
......RHVEDA.K........NAN.QP-....S.A....D....------   Rd
...-----KQAP.LDKKQ.KVGSVAITIDNGI.AGNKKIS..A.GSSANDA   4223
....GKVDKK.P.LDKKQ.QVG.VKIT.DSGINAGDQKISNVKDATDDTDA   LES-1
...*        *    **            *       *

        130       140       150       160                 ...
GWVVSTKNSTKEE-SNQVKQADEVLFEG-KDGVTVTSKSENGKHTVT---------------...
R.SFKSAKEGTG.QEGTTEV------------------------------------------...
...L.S..G.RN.K.Y.........T.-SGAA..S.S.KD....I.---------------...
...L.S..G.RN.K.Y.........T.-SGAA..S.S.KD....I.---------------...
```

09/936362

FIG.28H

```
...L.S..G.RN.K.Q...H........-................. ----------------...
...L.S..G.RN.K.Q...H........-.G..Q...T......I.----------------...
........GKEN.K.Q..........K.S.G..Q...T.....AI.----------------...
........G....-............T.-AGAA...........I.VSVAETKADCGLEKD...
........G....-............T.-AGAA...........I.VSVAETKADSGLEKD...
........G....-............T.-AGAA...........I.VSVAETKADSGLEKD...
VTIEQL.AAKPTLNAGAGISVTPTEISVDAKSGN..APTY.IGVKT.ELNSDGTSDKFSVKG...
VTYKQL.----------------------------------------------------------...
                           *  *** * *     *    ** **    *  ...

...
...----------------------------------------------------   33
...----------------------------------------------------   32
...----------------------------------------------------   29
...----------------------------------------------------   K22
...----------------------------------------------------   M4071
...----------------------------------------------------   11
...----------------------------------------------------   K9
...GDTIKLKVDNQNTDNVLTVGNNGTAVTKGGFETVKTGATDADRGKVT   HSF
...GDTIKLKVDNQNTDNVLTVGNNGTAVTKGGFETVKTGATDADRGKVT   API
...GDTIKLKVDNQNTDNVLTVGNNGTAVTKGGFETVKTGATDADRGKVT   Rd
...SGTNNSLVTAEHLASYLNEVNRTADSALQSF-TVKEED-DDDANAIT   4223
...-------------------QVQQDADGALQSF-SIRDEK-GQEFTISN   LES-1
...* *    * *     *   *  *     ******   * *

----------------------------------------------------------------...
```

FIG.28I

```
_____...                                                    33
_____...                                                    32
_____...                                                    29
_____...                                                    K22
_____...                                                    M4071
_____...                                                    11
_____...                                                    R9
VKDATANDADKKVATVKDVATALNSAATFVKTENLITSIDEDNPTDNGKDDALKAGDTLITFK...  HSF
VKDATANDADKKVATVKDVATALNSAATFVKTENLITSIDEDNPTDNGKDDALKAGDTLITFK...  API
VKDATANDADKKVATVKDVATALNSAATFVKTENLITTALDEPADAKDQG-DDALKAGDTLITFK...  Rd
VAKDTTKNAGAVSILKLKGKNGLTVAITKKD-GTVIFGLSQDSGLITGKSTLANNDGLTVKCDTN...  4223
LYSNKNTNTFETTTFA-GENGISISNDIAKGKVMVGIDPTNGLITPKLTVGSDKDGKTQLV...  LES-1
* *  ** *  **  *                                            ...
```

FIG.28J

```
------------------------------------------------------------...
------------------------------------------------------------...
------------------------------------------------------------...
------------------------------------------------------------...
------------------------------------------------------------...
------------------------------------------------------------...
------------------------------------------------------------...
PKVNITSPADGLNFAKETADASGSKNWYLKGIATTLTEPSAGAKSSHVDLNVDATK-KSNAA...
PKVNITSPADGLNFAKETADASGSKNWYLKGIATTLTEPSAGAKSSHVDLNVDATK-KSNAA...
------------------------------------------------------------...
PYLDQDKLQVGNVKITNTGTNAGGKATTGLSPTLPSIADQSS-RNILELGNTT-QDKQDKSNAA...
------------------------------------------GLSPTL[SITNAGGVRTTEQGNTITTSDEDKSKAA...
* **    *   ***  **** *  * *     ** * .  *   *** **...
```

```
...------------------------------------------------------------ 33
...------------------------------------------------------------ 32
...------------------------------------------------------------ 29
...------------------------------------------------------------ K22
...------------------------------------------------------------ M4071
...------------------------------------------------------------ 11
...------------------------------------------------------------ K9
...SIEDVLRAGAITNQGNGANMVDYVATYDTVNFTDDSTGTTTVTVTQKADG HSF
...SIEDVLRAGAITNQGNGANMVDYVATYDTVNFTDDSTGTTTVTVTQKADG API
...------------------------------------------------------------ Rd
...SINDITNTGFNLKNNSNSVGFVSTYNTVDFTDGNATTAKVTY-DEINQ 4223
...SIGDILNTGFNLKNNSNSVGFVSTYNTVDFTDGNATTAKVTY-TEINQ LES-1
```

09/936362

FIG.28K

```
                    ...** *** *****  * * * ****** *** *  **** ***  * **

---------------------------------------------------------------...
---------------------------------------------------------------...
---------------------------------------------------------------...
---------------------------------------------------------------...
---------------------------------------------------------------...
---------------------------------------------------------------...
---------------------------------------------------------------...
KGADVKIGAKTSVIKDHNGKLFTGKDLKDANNGATVSEDDGKDTGTGLVTAKTVIDAVNKSG...
KGADVKIGAKTSVIKDHNGKLFTGKDLKDANNGATVSEDDGKDTGTGLVTAKTVIDAVNKSG...
---------------------------------------------------------------...
TSKVVYDVNVDDTTIHLTGTDDNK-KLGVKTTKLNKTDANGNTATNFNVNSSDEDALVNAKD...
TSKVTYDVNVDEKTIELTGDNGKTNKIGVKTTTLTTINANGK-ATNF-STTDNDALVNAKDI...
 *                 *                  *  **  **   * *     **    ...
                   ...------------------------------------------------------  33
                   ...------------------------------------------------------  32
                   ...------------------------------------------------------  29
                   ...------------------------------------------------------  K22
                   ...------------------------------------------------------  M4071
                   ...------------------------------------------------------  11
                   ...------------------------------------------------------  K9
                   ...WRVTGEGATAETGATAVNAGNAETVTSGTSVNFKNGNATTATVSKDNGNIN  HSF
                   ...WRVTGEGATAETGATAVNAGNAETVTSGTSVNFKNGNATTATVSKDNGNIN  API
                   ...------------------------------------------------------  Rd
```

09/936362

FIG.28L

```
...IAENLNTLAKEIHTTKGTADTALQTFTVKKVDENNNADDANAIT-------   4223
...AENLNTLAKEIHTTKGTADTALQTFKVKK-----DGATDDETTT-------   LES-1
...      ** * *  **   *  *            *       ***

----------------------------------------------------...
----------------------------------------------------...
----------------------------------------------------...
----------------------------------------------------...
----------------------------------------------------...
----------------------------------------------------...
----------------------------------------------------...
VKYDVNVGDGLKIGDDKKIVADTTTLTVTGGKVSVPAGANSVNNNKKLVNAEGLATALNNLS...
VKYDVNVGDGLKIGDDKKIVADTTTLTVTGGKVSVPAGANSVNNNKKLVNAEGLATALNNLS...
----------------------------------------------------...
VGQKNANNQ--VNTLTLKGENGLNIKTDKNGTVTFGIN---------------------...
VGKDGTQNGKTVNTLKLKGENGLTVATNKDGTVTFGIN---------------------...
*            *   *        *   * **                        ...

...-------------------------------------------------   33
...-------------------------------------------------   32
...-------------------------------------------------   29
...-------------------------------------------------   K22
...-------------------------------------------------   M4071
...-------------------------------------------------   11
...-------------------------------------------------   K9
...WTAKADKYADGESEGETDQEVKAGDKVTF-KAGKNLKVKQSEKDFTYSLQD   HSF
```

09/936362

FIG.28M

```
...WTAKADKYADGESEGETDQEVKAGDKVTF-KAGKNLKVKQSEKDFTYSLQD   API
...--------------------------------------------------   Rd
...----------------TTSGLKAGKST-LNDGGLSIKNPTGSEQIQVGADG   4223
...----------------TQSGLKAGDSTTLNKDGKSIKNPASNEQIQVGADG   LES-1
...                *   ****       *  **   *  *   * *

-------------------------------------------------------...
-------------------------------------------------------...
-------------------------------------------------------...
-------------------------------------------------------...
-------------------------------------------------------...
-------------------------------------------------------...
-------------------------------------------------------...
TLTGLTSITLGGTANGRNDTGTVINKDGLTITLANGAAAGTDASNGNT----ISVTKDGISA...
TLTGLTSITLGGTANGRNDTGTVINKDGLTITLANGAAAGTDASNGNT----ISVTKDGISA...
-------------------------------------------------------...
VKFAKVNNNGVVGAGIDGTTRITRDEIGFTGTNGSLDKSKPHL------------SLDGINA...
VKFAKVDK-GNSSTGIDGTSRITKDQIGFTGANGSLDTTKPHLTKDKLKVGEVEITNTGINA...
   *        **     *    *  * * * *    *    *        * **  ** *...

...------------------------------   33
...------------------------------   32
...------------------------------   29
...------------------------------   K22
...------------------------------   M4071
...------------------------------   11
```

FIG.28N

```
...-------------------------------------------------------------...  K9
...GNKEITNVKSA----------LKTYKDTQNTA-------------------------------...  HSF
...GNKEITNVKSA----------LKTYKDTQNTA-------------------------------...  API
...-------------------------------------------------------------...  Rd
...GGKKITNTQSGEIAQNSHDAVTGGKTYDLKT--------------------------------...  4223
...GGKKITNTQSGDITQNSNDAVTGGRVYDLKT--------------------------------...  LES-1
...* * **** ******** *** *   * *

-------------------------------------------------------------...
-------------------------------------------------------------...
-------------------------------------------------------------...
-------------------------------------------------------------...
-------------------------------------------------------------...
-------------------------------------------------------------...
-------------------------------------------------------------...
-------------------------------------------------------DE...
GATQPAANTAEVAKQDLVDLITKPAITGAAGNGADAKAPDTTAATVGDLRGLGAVLSAKKTADE...
-------------------------------------------------------------...
-------------------------------------------------------EL...
-------------------------------------------------------EL...
-------------------------------------------------------EL...
                                                      *  ...

...-------------------------------------------------------------...  33
...-------------------------------------------------------------...  32
...-------------------------------------------------------------...  29
...-------------------------------------------------------------...  K22
...-------------------------------------------------------------...
```

FIG.28O

```
...------------------------------------------------------------  M4071
...------------------------------------------------------------  11
...------------------------------------------------------------  K9
...------------------------------------------------------------  HSF
...TQDKEFHAAVKNANEVVEFVGKNGATVSAKT                               SPI
...TQDKEFHAAVKNANEVVEFVGKNGATVSAKT                               Rd
...------------------------------------------------------------  4223
...ESKTNSAAKTAQNSLHEFSVADEQGNNFTV                                LES-1
...      *   *   **   *   *
------------------------------------------------------------...
------------------------------------------------------------...
-----------------------------------------ISVTKGSSFAEVKT...
-----------------------------------------ISVTKGSSFAEVKT...
------------------------------------------------------------...
------------------------------------------------------------...
DNNGKHTVTIDVAEAKVGDGLEKDTDGKIKLIVNITGNNLLTVDATKGASVAKGEFNAVTT...
DNNGKHTVTIDVAEAKVGDGLEKDTDGKIKLIVNITGNNLLTVDATKGASVAKGEFNAVTT...
SNPYSSVDTSKTSDVITFAGENGLITTKVMKGVVAVGIDQTKGLITTPKLTVGNNNGKGIVIDS...
SNPYSSVDTSKTSDVITFAGENGIITTKVMKGVVAVGIDQTKGLITTPKLTVGNNNGKGIVIDS...
*   *  **   * * *   * * * *           * *       * * *...
...------------------------------------------------------------  33
...------------------------------------------------------------  32
...------------------------------------------------------------  29
...DATTGGQVNAD-RGKVK----AEDENGADVDKKV------
```

186/204

09/936362

FIG.28P

```
...DATTGGQVNAD-RGKVK----AEDENGADVDKKV-------        K22
...-----------------------------------------        M4071
...-----------------------------------------        11
...-----------------------------------------        K9
...DATTAQGTNANERGKVVVKGSNGATATETDKKKV-------        HSF
...DATTAQGTNANERGKVVVKGSNGATATETDKKKV-------        API
...QNGQNTITGLSNTLANVTNDKGSVRTTEQGNIIKDEDKTRA        Rd
...KDGQNTITGLSNTLANVTNDGAGHSLS-QGLAN-DTDKTRA        LES-1
                                *
...

                                                                          ...
--------------------------------------------------------------------------...
                             INLNTDSSGNAVGSSTITFKAGDNLKIKQSGN...
ATVKDVAKAINDAATFVKVESTDDDIENGAAGKNETTDQALKAGDTLTLKAGKNLKAKLDQN...
ATVKDVAKAINDAATFVKVESTDDDIENGAAGKNETTDQALKAGDTLTLKAGKNLKAKLDQN...
--------------------------------------------------------------------------...
--------------------------------------------------------------------------...
--------------------------------------------------------------------------...
ATVGDVAKAINDAATFVKVEN-DDSATIDDSPTDDGANDALKAGDTLTLKAGKNLKVKRDG-...
ATVGDVAKAINDAATFVKVEN-DDSATIDDSPTDDGANDALKAGDTLTLKAGKNLKVKRDG-...
--------------------------------------------------------------------------...
ASIVDVLSAGFNLQGNGEAVDFVSTYDTVNFADGNATTAKVTYDDTSKTSKVVYDVNVDDTT...
ASIGDVLNAGFNLQGNGEAVDFVSTYDTVDFIDGNATTAKVTYDDTSKTSKVVYDVNVDNKT...
*** *       *     *                    *            *
                                ...        170        180        190        200
```

FIG.28Q

```
...-----FALANDLNVKNATVSDKLSLGANGKKVDITSDANG-------   33
...D--FTYS.KKE.KNLTSVETE...F....N..........-------   32
...GKSVT....K..D.TS.K......I.KDIN..........-------   29
...GKSVT....K..D.TS.K......I.KDIN..........-------   K22
...-----.T.EK..................N.......T..-------   M4071
...-----....K..G..T.....T.TI.GGAAAGAT.TPKVNVTSTTDG   11
...-----....K..SMRT.....T.TI.GSTTTGSA.TPKVNVTSTASG   K9
...-KNIT.......S..S..........T..N..N....TK.-------   HSF
...-KNIT.......S..S..........T..N..N....TK.-------   API
...-------------------------...N.......T..-------   Rd
...IEVK-DKKLGVKTTTTLTSTGTGANKFALSNQATGDALVKASDIVA--   4223
...IEVTSDKKLGVKTTTTLTKTSANGNATKFSA-ADGDALVKASDIAT--   LES-1
...                 *  *        *      *

          210         220        230        240         250      ...
LKFAKQGT-NGQNGN--VHLNGIASTLDDPRVGGKTAHLTKEISDTERN--RAASVGDVLNA...
..L..T.NG....S.--..........T.TLA.T.G.VDTN.DAVNYH--......Q....S...
..L..T.NG......--..........T.TIT.MT.QASNGVAVQ-NH--......A........
..L..T.NG......--..........T.TIT.MT.QASNGVAVQ-NH--......A........
.....PS.-......--..........T.TIT.TTKSATNGVDVQNH-.--.....A........
.....DAA--.A..DTT......G...T.TK..SPAT.IDGGDQS.HYT--....IK........
.V...GA.GANGDTT--...TN.....Q.TLLNTGVVSKLDGNGITADEKK.....Q....S...
.....DSKT-.DDA.--I.........T.TLLNSGATTNLGGNGITDNEKK.....K........
..x..DSKT-.DDA.--I.........T.TLLNSGATTNLGGNGITDNEKK.....K........
.....P..-......--...........................--..............
```

FIG.28R

```
------------------...TLSGDIQTAKGASQANNSAGYVDADGNKVIYDSTDNKYYQA...
------------------...TLSGDIQTAKGASQASSSASYVDADGNKVIYDSTDNKYYQV...
*  ***      **   ***  *** *                         **     *  ...
                                                  ...260       270       280       290       300
                                                  ...GMNIRGAK--TIGG-TVDNVDFVSTYDTVEFASGANANVSVTTDDN--     33
                                                  .......Q.NGNNVDFVR.Y.T....N---------.........A.TAH-     32
                                                  .......Q.NGASVDFVNAY.T....N---------.T.T..N....TAH-     29
                                                  .......Q.NGASVDFVNAY.T....N---------.T.T..N....TAH-     K22
                                                  .......Q.NGAS---------....N.....D.VN.L.T..N....TAHN     M4071
                                                  .......K.V.AGSTT-GQSE.....H.......L.-.DTETTTV.V.S--     11
                                                  .......K.V.TGAT---.S......R.......L..SEETTL..V.S---     K9
                                                  ......V..V.PASANNQ-.E.I...A.....D.V..DKDTT...VES---     HSF
                                                  ......V..V.PASANNQ-.E.I...A.....D.V..DKDTT...VES---     API
                                                  ...........--....-..............................--     Rd
                                                  ...KNDGTVD.TKEVAKDKLVAQAQTPDGTLAQMNVKSVI.KEQVN.A.--     4223
                                                  ...NDKGQVD.NKEVAKDKLVAQAQTPDGTLAQMNVKSVI.KEQVN.A.--     LES-1
                                                  ...                                  *

        310        320        330        340        350        360 ...
KKTTVRVDVTGLPVQYVTEDSKTVVKVGNEYYEAKQDGSADMDKKV-ENGKLAKTKVKLVSA...
...................G..........K..D.....NQ..-...E.............
...................G.....D.K...............-...E.............
...................G.....D.K...............-...E.............
...................GE......................-.................
            ..F.....G......................-K..E.V...........
```

FIG.28S

```
.ENGK.TE.KIGAKTS.IKEKDGKLFT.KANK.TNKVDG.NATEDA-DE..GLV.AKDVID....
ESNGKSTK.KIGAKTSGIKEKDGKLFT.KANKDTN.VASNNAADDT-DE..GLV.AETVIN....
.DNGK.TE.KIGAKTS.IK.HNGKLFT.K.LKD.NNN.VTVTETDGKDE.NGLV.AKAVID....
.DNGK.TE.KIGAKTS.IK.HNGKLFT.K.LKD.NNN.VTVTETDGKDE.NGLV.AKAVID....
.........................................-..................
..QGINEDNAFVKGLEKAASDNKTKNAAVTVGDLNAVAQTPLTFAG-DT.TT..KLGETLTI...
..QGINEDNAFIKGLENAAKDTKTKNAAVTVGDLNAVAQTPLTFAG-DT.TT..KLGETLTI...
** *                                             *         *    ...

                         ...     370       380       390       400
                         ...NGTNPVKISNVADGTEDTDAVSFKQLKALQDKQVTLSAS      33
                         ...S.............................T.      32
                         ...S.Q........E...EN...........E.....T..      29
                         ...S.Q........E...EN...........E.....T..      K22
                         ..................N....................      M4071
                         ..............E................N........      12
                         ...VNKTGWR.KTTDANGQNG.---FATVASGTNVTF---..      11
                         ...VNKAGWR.KTTGANNQAGQ---FETVTSGTNVTF---.D      K9
                         ...VNKAGWRVKTTGANGQND.---FATVASGTNVTF---.D      HSF
                         ...VNKAGWRVKTTGANGQND.---FATVASGTNVTF---.D      API
                         ......................................      Rd
                         ...KGGQTDTNKLTDNNIGVVAGTDGFTV.LAK.LTNLN.VN      4223
                         ...KGGQTDTNKLTDNNIGVVAGTDGFTV.LAK.LTNLN.VN      LESS-1
                         ...                            *     *

     410       420       430       440       450       460   ...
```

FIG.28T

```
NAYANGGSDADGGKATQTLGNDLNFKFKSTDSELLNIKAAGDTVTFTPKKGSVQVGDDGKAT...
.......T.N.........S.G.......S.G...K.S.T....................S...
.......N...........N.G.........G.....VEN...............E........
.......N...........N.G.........G.....VEN...............E........
..............GI...S.G.........G......EN........................
...........V..V....S.G.........G......DK....I.---------------...
GNGTTATVING-TDGITVKYDAKVGDGLKLDGD-KIAADTTALTVNDGKNANNPKGKVADVA...
GNGTTAVVTGDATNGITVKYEAKVGDGLKIGNDQKITADTTALTVTGGK--------VTAPD...
GNGTTAEVTKANDGSITVKYNVKVADGLKLDGD-KIVADTTVLTVADGK--------VTAPN...
GNGTTAEVTKANDGSITVKYNVKVADGLKLDGD-KIVADTTVLTVADGK--------VTAPN...
..............G....S.G.........G......EN........................
AGGTKIDDKGVSF--------------------------------------------------...
AGGTRIDEKGISFVDANGQAKANTPVLSANGLDLGGKRISNIGAAVDDNDAVNFKQFNEVAK...
   *                              *                  *          ...

     ...     470         480         490          500
     ...IQDGAKTTTGLVEASELVDSLNKLGWKVGVGKDGTG---AT              33
     ....SK..N..E.........E...........E.V.S.---EL              32
     .....N.T...D.........E...........D...S.---EL              29
     .....N.T...D.........E...........D...S.---E.              K22
     ................................T.T....V.---              M4071
     ...-----------------------------------------              12
     ...STDEKK----..T.KG..TA..S.S.TTTAAEADG.---TL              11
     ...ATNGKK----..N..G.A.A....S.TAK-AEADTANGGEL              K9
     ...NGDGKK----F.D..G.A.A....S.TATA..E...---EV              HSF
     ...NGDGKK----F.D..G.A.A....S.TATA..E...---EV              API
```

FIG.28U

```
                          ......................................---..   Rd
                          ...---------------------------------------   4223
                          ...TVNNLNNQSNSGASLPFVVTDANGKPIN.TDGKPQKAIKGA   LES-1
                          ...              *     *

        510       520       530       540       550       560 ...
DGTHTD-TLVKSGDKVTLKAGDNLKVKQEGTNFTYVLRDELTGVKSVEFKDTENGANGASTK...
...SKE-.........................A.K.............A...........
..ASNE-.............E.....D.....A.K.............A..S........
..ASNE-.............E.....D.....A.K.............A..S........
......-.........................A.K...D.........A...........
-------------------------------------------------------------...
..NASE-QE..A.....F...K........A....S.Q.A...LT.ITLGTGN...K---.E...
...ADE-KE..A.ET..F...K........A....S.Q.A...LT.ITLGTGN...K---.E...
.PANSAGQE..A.....F.......I..S.KD...S.KK..KDLT......ANG.TGSE......
.PANSAGQE..A.....F.......I..S.KD...S.KK..KDLT......ANG.TGSE......
......-.........................................................
-------------------------------------------------------------...
..KYYH-----------------------------------------------..ANGVP...
**                                                   * * *  ...
                          ...      570       580       590       600
                          ...ITKDGLTITPAND-ANGAAATDADKIK---VASDGISAGNKAV   33
                          ...........L..G-....TV.......---............   32
                          ...........S..G-.............---............   29
                          ...........S..G-.............---............   K22
```

09/936362

FIG.28V

```
                  ...............G-.GA.G.NT.NT.S---.TK..........  M4071
                  ...---------R.SG-............---.............  12
                  ....N.........G-.---G.NN.NT.S---.TK......DQS.  11
                  ....N.........G-----G.NN.NT.S---.TK......DQS.  K9
                  ...............G-.GA.G.NT.NT,S---.TK..........  HSF
                  ...............G-.GA.G.NT.NT,S---.TK..........  API
                  ..........F...G-............---......R......  Rd
                  ...-------------------------------------------  4223
                  ...VD...KP..D.DKL..L..HGKPLDAGHQV...L.-GNSD-.I  LES-1
                  ...* ***  ** *   *  **          **  * * *  **

    610       620       630       640       650       660   ...
KNVVSGLKKFGDANFNPLTSSADNLTKQYDNAYKGLTNLDEKSKGKQTPTVADNTAATVGDL...
--------------------------------------------------------------...
............................D..........GAD...L................
............................D..........GAD...L................
..............D...............................................
.-------------------------------------------------------------...
..............D...........N.D..........GTD....V...............
..............  ............D..........GAD...L................
T..........GHTLANGTV..FE-.H.......D.....GADNN-.................
T..........GHTLANGTV..FE-.H......XD.....GADNN-.................
--------------------------------------------------------------...
--------------------------------------------------------------...
----------------TLTNIKSTLP.I.TPNT.NA.AGQAQSLPSLSAAQQSN..S.K.V...
```

09/936362

FIG.28W

```
      *         *      **  *           *  ****  **...
...     670         680         690        700
...TGLGWVISADKTTGES-KEYSAQVRNANEVKFKSGNGIN     33
...-------------------------------------     32
.................LN...N................H     29
.................LN...N................H     K22
..............K..LN...N.................     M4071
...-------------------------------------     12
................G.-T..HD................     11
.................LD...N.................     K9
.................PNQ..N.................     HSF
.................PNQ..N.................     API
...-------------------------------------     Rd
...-------------------------------------     4223
...LNV.FNLQTNHNQVDFV.A.DTVNFVNGTGADITSVRSA     LES-1
...  *** * **          *             **

     710        720        730        740        750        760  ...
VSGKTLDNGTREITFELAKDENAIAFGSGSKALRDNTVAIGTGNVVNAEKSGAFGDPNYIED...
-------------------------------------------------------------...
-----V-..R................Y...................................
-----V-..R................Y...................................
..............................................................
-------------------------------------------------------------...
.....V-..R........G.-----------------------------------------...
```

FIG.28X

```
.....V-..R........G.---------------------------------------...
......-....V.......G.---------------------------------------...
......-....V.......G.---------------------------------------...
-----------------------------------------------------------...
-----------------------------------------------------------...
DGTMSNITVNTALAATDDDGNVL.KAKD.KFYKA.DLMPN.SLKAGKSASDAKTPTGLSLVN...
 ** *       **      *   *        ** *  **      *    *       * *...

                         ...   770       780       790       800
                         ...KAGGSYAFGNDNRITSKNTFVLGNGVNAKYKANGKVDT-----     33
                         ...------------------------------------------     32
                         .............................................     29
                         .............................................     K22
                         ...........................S....RD...N.L.EE---     M4071
                         ...------------------------------------------     12
                         ...------------------------------------------     11
                         ...------------------------------------------     K9
                         ...------------------------------------------     HSF
                         ...------------------------------------------     API
                         ...------------------------------------------     Rd
                         ...------------------------------------------     4223
                         ...PNA.KGST.DAVALNNLSKA.FKSKDGTTTTTVSSDGISIQGK    LES-1
                         ...   **  * **   *      *      *   * *

-----------------------------------------------------------...
-----------------------------------------------------------...
```

FIG.28Y

```
-------------------------------------------------------------...
-------------------------------------------------------------...
-------------------------------------------------------------...
-------------------------------------------------------------...
VVKSNEFTVKETNGKETSLVKVGDLYYSKEDIDLTTGQPKLKDGNTVAAKYQDKGGKVVS-V...
VVKSNEFTVKETNGKETSLVKVGDLYYSKEDIDPATGKPKVTNGNAVAAKYQDKDGKVVSAD...
VVKSNEFTVKNADGSETNLVKVGDLYYSKEDIDPATSKPMTGKTE----KYKVENGKVVSAN ...
VVKSNEFTVKNADGSETNLVKVGDLYYSKEDIDPATSKPMTGKTE----KYKVENGKVVSAN...
-------------------------------------------------------------...
VDSSGQAKANTPVLSANGLDLGGKVISNVGKGTKDTDAANVQQLNEVRNLLGLGNAGNDNAD...
DNSSI-------TLSKDGLNVGGKVISNVGKGTKDTDAANVQQLNEVRNLLGLGNAGNDNAD...
   * *             *   *              *        * *        *    **...
...-------------------------------------   33
...-------------------------------------   32
...-------------------------------------   29
...-------------------------------------   K22
...-------------------------------------   M4071
...-------------------------------------   12
...TDNTEATITNKGSGYVTGNQ-----------------   11
...GSSNTAVTLTNKGYGYVTGNQ----------------   K9
...GSK-TEVTLTMKGSGYVTGNQ----------------   HSF
...GSK-TEVTLTMKGSGYVTGNQ----------------   API
...-------------------------------------   Rd
...GNQVNIADIKKDPNSGSSSNRTVIKAGTVLGGKGNNDT   4223
...GNQVNIADIKKDPNSGSSSNRTVIKAGTVLGGKGNNDT   LES-1
```

FIG.28Z

```
                        ...          *       ***

--------------------------------------------------------------...
--------------------------------------------------------------...
--------------------------------------------------------------...
--------------------------------------------------------------...
--------------------------------------------------------------...
--------------------------------------------------------------...
VADAIAKSGFEKGKADEADAKRAFDD--KTKALSAGTTE-IVNAHDKVRFANGLNTKVSAAT...
VADAIAKSGFEKGKADAEKAKAAFGD--ETKALSSDKLE-TVNANDKVRFANGLNTKVSAAT...
VADAIAKSGFEKGKADAAEAEKAFAESAKDKQLSKDKAE-TVNAHDKVRFANGLNTKVSAAT...
VADAIAKSGFEKGKADAAEAEKAFAESAKDKQLSKDKAE-TVNAHDKVRFANGLNTKVSAAT...
--------------------------------------------------------------...
EKLATGGIQVGVDKDGNANGDLSNVWVKTQKDGSKKALLATYNAAGQTNYLTNNPAEAIDRI...
EKLATGGVQVGVDKDGNANGDLSNVWVKTQKDGSKKALLATYNAAGQTNYLTNNPAEAIDRI...
  * *    *    * *      * *   * **   *    *                      ...
                           ...----------------------------------------   33
                           ...----------------------------------------   32
                           ...----------------------------------------   29
                           ...----------------------------------------   K22
                           ...----------------------------------------   M4071
                           ...----------------------------------------   12
                           ...VESTDANGDKVTTTFVKTDVELPLTQIYNTDANGKKITKVV   11
                           ...VESTDANGDKVTTTFVKTDVELPLTQIYNTDANGKKI---V   K9
                           ...VESTDANGDKVTTTFVKTDVELPLTQIYNTDANGNKI---V   HSF
```

FIG.28A'

```
...VESTDANGDKVTTTFVKTDVELPLTQIYNTDANGNKI---V    API
...-----------------------------------------    Rd
...NEQGIRFFHVNDGNQEPVVQGRNGIDSSASGKHSVAIGFQ-    4223
...NEQGIRFFHVNDGNQEPVVQGRNGIDSSASGKHSVAIGFQ-    LES-1
...  * *       *           *   *   *  **

----------------------------------------------------------...
----------------------------------------------------------...
----------------------------------------------------------...
----------------------------------------------------------...
----------------------------------------------------------...
----------------------------------------------------------...
KDGQTKWYELNADGTADMTKEVTLGNVDSDGKKVVKDNDG---KWYHAKADGTADKTKGEVD...
KNGD-KWYYTKDDGSTDMTKEVTLGNVDSDGKKVVKEDN----KWYGVKSDGSTDKTQVVEE...
KKADGKWYELNADGTASN-KEVTLGNVDANGKKVVKVTENGADKWYYTNADGAADKTKGEVS...
KKADGKWYELNADGTASN-KEVTLGNVDANGKKVVKVTENGADKWYYTNADGAADKTKGEVS...
----------------------------------------------------------...
AKADGEAAVAIGRQTQAGNQSIAIGDNAQATGDQSIAIGTGNVVAGKHSGAIGDPSTVKADN...
AKADGEAAVAIGRQTQAGNQSIAIGDNAQATGDQSIAIGTGNVVTGKHSGAIGDPSTVKADN...
  **        *     *****    *        *        *  *   *       ...
                    ...------------------------    33
                    ...------------------------    32
                    ...------------------------    29
                    ...------------------------    K22
                    ...------------------------    M4071
```

FIG.28B'

```
...------------------------------         12
...NDKVSTDEKHVVSLDPNDQSKGKGVV             11
...A-KVSTDEKHVVSLDPNDQSKGKGVV             K9
...NDKVSTDEKHVVSLDPNDQSKGKGVV             HSF
...NDKVSTDEKHVVSLDPNDQSKGKGVV             API
...------------------------------         Rd
...SYSVGNNNQGTDATQTDVFGVGNNIT             4223
...SYSVGNNNQGTDATQTDVFGVGNNIT             LES-1
...    ** **       * *  * *  *

      810       820       830        840      850       860 ...
ETVTVKDKDGKETTVTVPKALGATVENSVYLGNKSTATKDKGKNLKSDGTAGNTTTAGTTGT...
------------------------------------------------------------...
.................................................................
.................................................................
.EKE.VG..AK.K...Q...E...........A.......................A.....
------------------------------------------------------------...
------------------------------------------------------------...
------------------------------------------------------------...
------------------------------------------------------------...
------------------------------------------------------------...
------------------------------------------------------------...
VTESNSVAL.SNSAISAGTHA.TQAK------------------.......T.....A.....
VTESNSVAL.SNSAISAGTHA.TQAK------------------.......T.....A.....
        *  * **     *                      ******* *********...
                                 ...     870       880       890       900
                                 ...VNGFAGATAHGAVSVGASGEERRIQNVAAGEISATSTD     33
                                 ...------------------------K.............     32
                                 .........................................     29
```

FIG.28C'

```
...........................................    K22
...........................................    M4071
...------------------------..............      12
...------------------------.D..N.D......       11
...------------------------.N.M.N.........     K9
...------------------------.D..N.........      HSF
...------------------------.D..N.........      API
...------------------------K.............      Rd
....K...Q..V.........A..........V.....         4223
....K...Q..V.........A..........V.....         LES-1
...* **** ** ********* **** *** *********

        910       920                930       940       950    ...
AINGSQLYAVAKGVTNLAGQVN-------KVGKRADAGTASALAASQLPQASMSGKSMVSIA...
......................NLEGKVN.....................T.P...........
......................-------.......................P...........
......................-------.......................P...........
......................-------.......................P...........
......................-------.......................P...........
......................NLEGKVN.....................T.P.....A.....
......................NLEGKVN.....................T.P...........
......................NLEGKVN.....................T.P.....A.....
......................NLEGKVN.....................T.P.....A.....
......................-------.......................P...........
.V.....---.ATQSI.NAT.ELDHRIHQNENK.N..IS..M.MASM...YIP.R...TGG...
.V.....---.ATQGI.NAT.ELDHRIHQNENK.N..IS..M.MASM...YIP.R...TGG...
********   **   **   *          ***** ***** * ****   ****** *...
```

FIG.28D'

```
...  960       970       980       990      1000
...GSSYQGQSGLAIGVSRISDNGKVIIRLSGTTNSQGKTGVAAGVGYQW*     33
.........N.......................................*     32
.........N.......................................*     29
.........N.......................................*     K22
.................................................*     M4071
.......................L.........................*     12
.........N.......................................*     11
.........N.......................................*     K9
.........N.......................................*     HSF
.........N.......................................*     API
.................................................*     Rd
...IATHN..GAV.V.L.KL....QWVFKIN.SADT..HV.A.V.A.FHF*     4223
...IATHN..GAV.V.L.KL....QWVFKIN.SADT..HV.A.V.A.FHF*     LES-1
... ****** ************* * ** ******* * * * ** *
```

FIG.29

Oligonucleotides primers to PCR amplify truncated strain 11 S44 hia gene.

```
              Nde I
                 M  S44A  T  V  E  A  N  N  N  T                         SEQ ID NO:56
5'    GGGAATTCATATGTCCGCAACGGTTGAGGCGAACAACAATACT    3'        6817.SL     SEQ ID NO:55

                                      Sty I
       H  T  I  T  F  A  L  A  K  D  L  G                                  SEQ ID NO:59
      CACACCATTACCTTTGCTTTAGCGAAAGACCTTGGT                                 SEQ ID NO:58
3'    GTGTGGTAATGGAAACGAAATCGCTTTCTGGAACCACCCTAGGGC    5'      6818.SL     SEQ ID NO:57
```

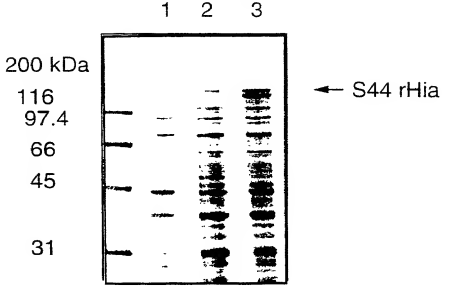
Construction of JB-2930-3, pBR T7/S44 hia(11)/cer/kanR
PCR amplify Nde-Sty S44 hia (11)
clone into pCR II
ApR
JB-2910-1-1
KanR
S44 5'hia
Nde
StyB
R Nde
PCR II/S44 5'hia
Nde/Sty
HXbBg
Nde
Nde/Sty
T7p
Ps
Ps
V38 hia(11)
IA-46-5
ApR
RSmBR
PUC T7 V38 hia(11)
Nde Sty
Ps
Ps
S44 hia(11)
JB-2917-1
ApR
RSmBR
PUC S44 hia(11)
Nde
Nde/CAP

FIG.30A

HXbBgNde Sty Ps Ps
Nde
T7p
S44 hia(11)
JB-2925-3
ApR
RSmBR
PUC T7 S44 hia(11)
Bg/B
Bg/CAP
PCR /MCS/tl/cer/kanR
H B B
Cer
SPs H
KanR
PsS
BK-2-1-2
RSmKXhoBgXbPs
H B B
Cer
SPs H
KanR
PsS
T7p
JB-2930-3
S44 hia(11)
BgXhoKSmR
Nde
Sty
Ps
Ps
RXbPs
PCR T7/S44 hia(11)/cer/kanR

FIG.30B

Production of S44 rHia from different vectors



1. pET S44 hia t_0
2. pET S44 hia t_4
3. pBR T7 S44 hia/cer/kanR t_4

FIG.31

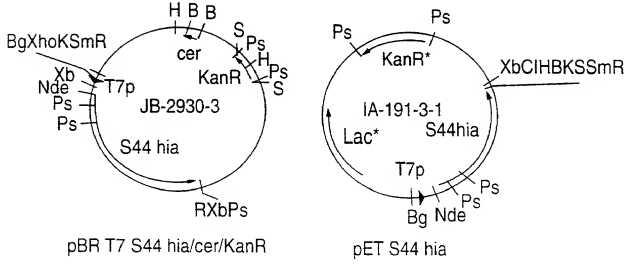


FIG.32

Docket No.
1038-1190 MS:jb

Declaration and Power of Attorney For Patent Application

English Language Declaration

As a below named inventor, I hereby declare that:

My residence, post office address and citizenship are as stated below next to my name,

I believe I am the original, first and sole inventor (if only one name is listed below) or an original, first and joint inventor (if plural names are listed below) of the subject matter which is claimed and for which a patent is sought on the invention entitled

RECOMBINANT HAEMOPHILUS INFLUENZAE ADHESIN PROTEINS

the specification of which
(check one)

☐ is attached hereto.

☒ was filed on **March 16, 2000** as United States Application No. or PCT International Application Number **PCT/CA00/00289**

and was amended on _____
(if applicable)

I hereby state that I have reviewed and understand the contents of the above identified specification, including the claims, as amended by any amendment referred to above.

I acknowledge the duty to disclose to the United States Patent and Trademark Office all information known to me to be material to patentability as defined in Title 37, Code of Federal Regulations, Section 1.56.

I hereby claim foreign priority benefits under Title 35, United States Code, Section 119(a)-(d) or Section 365(b) of any foreign application(s) for patent or inventor's certificate, or Section 365(a) of any PCT International application which designated at least one country other than the United States, listed below and have also identified below, by checking the box, any foreign application for patent or inventor's certificate or PCT International application having a filing date before that of the application on which priority is claimed.

Prior Foreign Application(s)			Priority Not Claimed
(Number)	(Country)	(Day/Month/Year Filed)	☐
(Number)	(Country)	(Day/Month/Year Filed)	☐
(Number)	(Country)	(Day/Month/Year Filed)	☐

I hereby claim the benefit under 35 U.S.C. Section 119(e) of any United States provisional application(s) listed below:

(Application Serial No.)	(Filing Date)
(Application Serial No.)	(Filing Date)
(Application Serial No.)	(Filing Date)

I hereby claim the benefit under 35 U. S. C. Section 120 of any United States application(s), or Section 365(c) of any PCT International application designating the United States, listed below and, insofar as the subject matter of each of the claims of this application is not disclosed in the prior United States or PCT International application in the manner provided by the first paragraph of 35 U.S.C. Section 112, I acknowledge the duty to disclose to the United States Patent and Trademark Office all information known to me to be material to patentability as defined in Title 37, C. F. R., Section 1.56 which became available between the filing date of the prior application and the national or PCT International filing date of this application:

09/268,347	**March 16, 1999**	**Pending**
(Application Serial No.)	(Filing Date)	(Status) (patented, pending, abandoned)
PCT/CA00/00289	**March 16, 2000**	
(Application Serial No.)	(Filing Date)	(Status) (patented, pending, abandoned)
(Application Serial No.)	(Filing Date)	(Status) (patented, pending, abandoned)

I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code and that such willful false statements may jeopardize the validity of the application or any patent issued thereon.

POWER OF ATTORNEY: As a named inventor, I hereby appoint the following attorney(s) and/or agent(s) to prosecute this application and transact all business in the Patent and Trademark Office connected therewith. *(list name and registration number)*

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Fifth inventor's signature

Date

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Full name of sixth inventor, if any

Sixth inventor's signature

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Citizenship

Post Office Address